

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
29 July 2004 (29.07.2004)

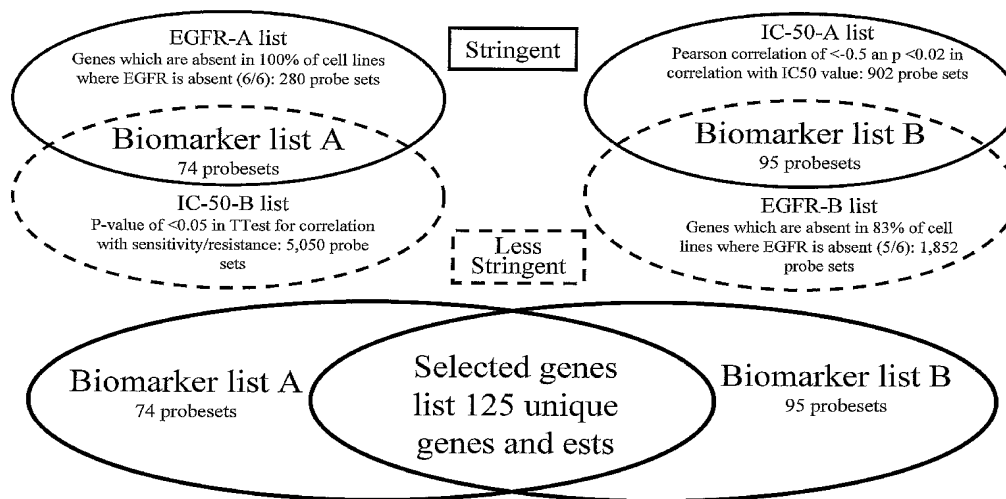
PCT

(10) International Publication Number
WO 2004/063709 A2

- (51) International Patent Classification⁷: **G01N**
- (21) International Application Number:
PCT/US2004/000368
- (22) International Filing Date: 8 January 2004 (08.01.2004)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
60/438,735 8 January 2003 (08.01.2003) US
- (71) Applicant (for all designated States except US): **BRISTOL-MYERS SQUIBB COMPANY** [US/US]; Route 206 and Province Line Road, Princeton, New Jersey 08543-4000 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): **AMLER, Lukas, C.** [US/US]; 845 Granada Lane, Foster City, California 94404 (US). **JANUARIO, Thomas** [US/US]; 11 South Main Street, Lambertville, New Jersey 08530 (US).
- (74) Agents: **GOLIAN, Paul, D.** et al.; Bristol-Myers Squibb Company, P.O. Box 4000, Princeton, New Jersey 08543-4000 (US).
- (81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.
- (84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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(54) Title: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO EPIDERMAL GROWTH FACTOR RECEPTOR MODULATORS



(57) Abstract: EGFR biomarkers useful in a method for identifying a mammal that will respond therapeutically to a method of treating cancer comprising administering an EGFR modulator, wherein the method comprises (a) exposing the mammal to the EGFR modulator and (b) measuring in the mammal level of at least one biomarker, wherein a difference in the level in at least one biomarker measured in (b) compared to the level of the biomarker in a mammal that has not been exposed to the EGFR modulator indicates that the mammal will respond therapeutically to the method of treating cancer.

**Declarations under Rule 4.17:**

- as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii)) for the following designations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, ARIPO patent (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG)
- as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii)) for the following designations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE,

EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, ARIPO patent (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG)

Published:

- without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO EPIDERMAL GROWTH FACTOR RECEPTOR MODULATORS

FIELD OF THE INVENTION

The present invention relates generally to the field of pharmacogenomics, and more specifically to methods and procedures to determine sensitivity in patients to allow the development of individualized genetic profiles which aid in treating diseases and disorders based on patient response at a molecular level.

BACKGROUND OF THE INVENTION:

Cancer is a disease with extensive histoclinical heterogeneity. Although conventional histological and clinical features have been correlated to prognosis, the same apparent prognostic type of tumors varies widely in its responsiveness to therapy and consequent survival of the patient.

New prognostic and predictive markers, which would facilitate an individualization of therapy for each patient, are needed to accurately predict patient response to treatments, such as small molecule or biological molecule drugs, in the clinic. The problem may be solved by the identification of new parameters that could better predict the patient's sensitivity to treatment. The classification of patient samples is a crucial aspect of cancer diagnosis and treatment. The association of a patient's response to a treatment with molecular and genetic markers can open up new opportunities for treatment development in non-responding patients, or distinguish a treatment's indication among other treatment choices because of higher confidence in the efficacy. Further, the pre-selection of patients who are likely to respond well to a medicine, drug, or combination therapy may reduce the number of patients needed in a clinical study or accelerate the time needed to complete a clinical development program (M. Cockett et al., 2000, *Current Opinion in Biotechnology*, 11:602-609).

The ability to predict drug sensitivity in patients is particularly challenging because drug responses reflect not only properties intrinsic to the target cells, but also a host's metabolic properties. Efforts to use genetic information to predict drug sensitivity have primarily focused on individual genes that have broad effects, such as the multidrug resistance genes, *mdr1* and *mrp1* (P. Sonneveld, 2000, *J. Intern. Med.*, 247:521-534).

The development of microarray technologies for large scale characterization of gene mRNA expression pattern has made it possible to systematically search for molecular markers and to categorize cancers into distinct subgroups not evident by traditional histopathological methods (J. Khan et al., 1998, *Cancer Res.*, 58:5009-5013; A.A. Alizadeh et al., 2000, *Nature*, 403:503-511; M. Bittner et al., 2000, *Nature*, 406:536-540; J. Khan et al., 2001, *Nature Medicine*, 7(6):673-679; and T.R. Golub et al., 1999, *Science*, 286:531-537; U. Alon et al., 1999, *Proc. Natl. Acad. Sci. USA*, 96:6745-6750). Such technologies and molecular tools have made it possible to monitor the expression level of a large number of transcripts within a cell population at any given time (see, e.g., Schena et al., 1995, *Science*, 270:467-470; Lockhart et al., 1996, *Nature Biotechnology*, 14:1675-1680; Blanchard et al., 1996, *Nature Biotechnology*, 14:1649; U.S. Patent No. 5,569,588 to Ashby et al.).

Recent studies demonstrate that gene expression information generated by microarray analysis of human tumors can predict clinical outcome (L.J. van't Veer et al., 2002, *Nature*, 415:530-536; M. West et al., 2001, *Proc. Natl. Acad. Sci. USA*, 98:11462-11467; T. Sorlie et al., 2001, *Proc. Natl. Acad. Sci. USA*, 98:10869-10874; M. Shipp et al., 2002, *Nature Medicine*, 8(1):68-74). These findings bring hope that cancer treatment will be vastly improved by better predicting the response of individual tumors to therapy.

Needed are new and alternative methods and procedures to determine drug sensitivity in patients to allow the development of individualized genetic profiles which are necessary to treat diseases and disorders based on patient response at a molecular level.

SUMMARY OF THE INVENTION:

The invention provides methods and procedures for determining patient sensitivity to one or more Epidermal Growth Factor Receptor (EGFR) modulators. The invention also provides methods of determining or predicting whether an individual requiring therapy for a disease state such as cancer will or will not respond to treatment, prior to administration of the treatment, wherein the treatment comprises one or more EGFR modulators. The one or more EGFR modulators are compounds that can be selected from, for example, one or more EGFR specific ligands, one or

more small molecule EGFR inhibitors, or one or more EGFR binding monoclonal antibodies.

In one aspect, the invention provides a method for identifying a mammal that will respond therapeutically to a method of treating cancer comprising administering an EGFR modulator, wherein the method comprises: (a) measuring in the mammal
5 the level of at least one biomarker selected from the biomarkers of Table 4; (b) exposing the mammal to the EGFR modulator; (c) following the exposing of step (b), measuring in the mammal the level of the at least one biomarker, wherein a difference in the level of the at least one biomarker measured in step (c) compared to the level of
10 the at least one biomarker measured in step (a) indicates that the mammal will respond therapeutically to said method of treating cancer.

As used herein, respond therapeutically refers to the alleviation or abrogation of the cancer. This means that the life expectancy of an individual affected with the cancer will be increased or that one or more of the symptoms of the cancer will be
15 reduced or ameliorated. The term encompasses a reduction in cancerous cell growth or tumor volume. Whether a mammal responds therapeutically can be measured by many methods well known in the art, such as PET imaging.

The at least one biomarker can also be selected from the biomarkers of Table 5. The mammal can be, for example, a human, rat, mouse, dog rabbit, pig sheep, cow,
20 horse, cat, primate, or monkey.

The method of the invention can be, for example, an in vitro method and wherein the at least one biomarker is measured in at least one mammalian biological sample from the mammal. The biological sample can comprise, for example, at least one of whole fresh blood, peripheral blood mononuclear cells, frozen whole blood,
25 fresh plasma, frozen plasma, urine, saliva, skin, hair follicle, or tumor tissue.

In another aspect, the invention provides a method for identifying a mammal that will respond therapeutically to a method of treating cancer comprising administering an EGFR modulator, wherein the method comprises: (a) exposing the mammal to the EGFR modulator; (b) following the exposing of step (a), measuring in
30 the mammal the level of the at least one biomarker selected from the biomarkers of Table 4, wherein a difference in the level of the at least one biomarker measured in step (b), compared to the level of the biomarker in a mammal that has not been

exposed to said EGFR modulator, indicates that the mammal will respond therapeutically to said method of treating cancer.

In yet another aspect, the invention provides a method for testing or predicting whether a mammal will respond therapeutically to a method of treating cancer comprising administering an EGFR modulator, wherein the method comprises: (a) measuring in the mammal the level of at least one biomarker selected from the biomarkers of Table 4; (b) exposing the mammal to the EGFR modulator; (c) following the exposing of step (b), measuring in the mammal the level of the at least one biomarker, wherein a difference in the level of the at least one biomarker measured in step (c) compared to the level of the at least one biomarker measured in step (a) indicates that the mammal will respond therapeutically to said method of treating cancer.

In another aspect, the invention provides a method for determining whether a compound inhibits EGFR activity in a mammal, comprising: (a) exposing the mammal to the compound; and (b) following the exposing of step (a), measuring in the mammal the level of at least one biomarker selected from the biomarkers of Table 4, wherein a difference in the level of said biomarker measured in step (b), compared to the level of the biomarker in a mammal that has not been exposed to said compound, indicates that the compound inhibits EGFR activity in the mammal.

In yet another aspect, the invention provides a method for determining whether a mammal has been exposed to a compound that inhibits EGFR activity, comprising (a) exposing the mammal to the compound; and (b) following the exposing of step (a), measuring in the mammal the level of at least one biomarker selected from the biomarkers of Table 4, wherein a difference in the level of said biomarker measured in step (b), compared to the level of the biomarker in a mammal that has not been exposed to said compound, indicates that the mammal has been exposed to a compound that inhibits EGFR activity.

In another aspect, the invention provides a method for determining whether a mammal is responding to a compound that inhibits EGFR activity, comprising (a) exposing the mammal to the compound; and (b) following the exposing of step (a), measuring in the mammal the level of at least one biomarker selected from the biomarkers of Table 4, wherein a difference in the level of said biomarker measured

in step (b), compared to the level of the biomarker in a mammal that has not been exposed to said compound, indicates that the mammal is responding to the compound that inhibits EGFR activity.

As used herein, “responding” encompasses responding by way of a biological and cellular response, as well as a clinical response (such as improved symptoms, a therapeutic effect, or an adverse event), in a mammal

The invention also provides an isolated biomarker selected from the biomarkers of Table 4. The biomarkers of the invention comprise sequences selected from the nucleotide and amino acid sequences provided in Table 4 and the Sequence Listing, as well as fragments and variants thereof.

The invention also provides a biomarker set comprising two or more biomarkers selected from the biomarkers of Table 4.

The invention also provides kits for determining or predicting whether a patient would be susceptible or resistant to a treatment that comprises one or more EGFR modulators. The patient may have a cancer or tumor such as, for example, a colon cancer or tumor.

In one aspect, the kit comprises a suitable container that comprises one or more specialized microarrays of the invention, one or more EGFR modulators for use in testing cells from patient tissue specimens or patient samples, and instructions for use. The kit may further comprise reagents or materials for monitoring the expression of a biomarker set at the level of mRNA or protein.

In another aspect, the invention provides a kit comprising two or more biomarkers selected from the biomarkers of Table 4.

In yet another aspect, the invention provides a kit comprising at least one of an antibody and a nucleic acid for detecting the presence of at least one of the biomarkers selected from the biomarkers of Table 4. In one aspect, the kit further comprises instructions for determining whether or not a mammal will respond therapeutically to a method of treating cancer comprising administering a compound that inhibits EGFR activity. In another aspect, the instructions comprise the steps of (a) measuring in the mammal the level of at least one biomarker selected from the biomarkers of Table 4, (b) exposing the mammal to the compound, (c) following the exposing of step (b), measuring in the mammal the level of the at least one biomarker,

wherein a difference in the level of the at least one biomarker measured in step (c) compared to the level of the at least one biomarker measured in step (a) indicates that the mammal will respond therapeutically to said method of treating cancer.

5 The invention also provides screening assays for determining if a patient will be susceptible or resistant to treatment with one or more EGFR modulators.

The invention also provides a method of monitoring the treatment of a patient having a disease treatable by one or more EGFR modulators.

10 The invention also provides individualized genetic profiles which are necessary to treat diseases and disorders based on patient response at a molecular level.

The invention also provides specialized microarrays, e.g., oligonucleotide microarrays or cDNA microarrays, comprising one or more biomarkers having expression profiles that correlate with either sensitivity or resistance to one or more EGFR modulators.

15 The invention also provides antibodies, including polyclonal or monoclonal, directed against one or more biomarkers of the invention.

The invention will be better understood upon a reading of the detailed description of the invention when considered in connection with the accompanying figures.

20

BRIEF DESCRIPTION OF THE FIGURES:

FIG. 1 illustrates a EGFR biomarker identification and prioritization strategy.

25 FIG. 2A illustrates the RT-PCR results for EGFR in thirty one colon cancer cell lines to identify cell lines which do not have significant mRNA expression of EGFR.

FIG. 2B illustrates the IC₅₀ profile for twenty two colon cancer cell lines with an EGFR inhibitor compound, and determination of sensitive and resistant cell lines.

DETAILED DESCRIPTION OF THE INVENTION:

The invention provides biomarkers that respond to the modulation of a specific signal transduction pathway and also correlate with EGFR modulator sensitivity or resistance. These biomarkers can be employed for predicting response to one or more EGFR modulators. In one aspect, the biomarkers of the invention are those provided in Table 4 and the Sequence Listing, including both polynucleotide and polypeptide sequences.

The biomarkers were determined by an *in vitro* assay employing microarray technology to monitor simultaneously the expression pattern of thousands of discrete genes in untreated cells, whose response to the modulation of a signal transduction pathway, in particular the EGFR pathway, was tested on untreated cells whose sensitivity to EGFR modulators was tested. The biomarkers have expression levels in the cells that are dependent on the activity of the EGFR signal transduction pathway and that are also highly correlated with EGFR modulator sensitivity exhibited by the cells. Biomarkers serve as useful molecular tools for predicting a response to EGFR modulators, preferably biological molecules, small molecules, and the like that affect EGFR kinase activity via direct or indirect inhibition or antagonism of EGFR kinase function or activity.

EGFR MODULATORS

As used herein, the term "EGFR modulator" is intended to mean a compound or drug that is a biological molecule or a small molecule that directly or indirectly modulates EGFR activity or the EGFR signal transduction pathway. Thus, compounds or drugs as used herein is intended to include both small molecules and biological molecules. Direct or indirect modulation includes activation or inhibition of EGFR activity or the EGFR signal transduction pathway. In one aspect, inhibition refers to inhibition of the binding of EGFR to an EGFR ligand such as, for example, EGF. In another aspect, inhibition refers to inhibition of the kinase activity of EGFR.

EGFR modulators include, for example, EGFR specific ligands, small molecule EGFR inhibitors, and EGFR monoclonal antibodies. In one aspect, the EGFR modulator inhibits EGFR activity and/or inhibits the EGFR signal transduction

pathway. In another aspect, the EGFR modulator is an EGFR antibody that inhibits EGFR activity and/or inhibits the EGFR signal transduction pathway.

EGFR modulators include biological molecules or small molecules.

Biological molecules include all lipids and polymers of monosaccharides, amino
5 acids, and nucleotides having a molecular weight greater than 450. Thus, biological molecules include, for example, oligosaccharides and polysaccharides; oligopeptides, polypeptides, peptides, and proteins; and oligonucleotides and polynucleotides. Oligonucleotides and polynucleotides include, for example, DNA and RNA.

Biological molecules further include derivatives of any of the molecules
10 described above. For example, derivatives of biological molecules include lipid and glycosylation derivatives of oligopeptides, polypeptides, peptides, and proteins.

Derivatives of biological molecules further include lipid derivatives of oligosaccharides and polysaccharides, e.g., lipopolysaccharides. Most typically, biological molecules are antibodies, or functional equivalents of antibodies.
15 Functional equivalents of antibodies have binding characteristics comparable to those of antibodies, and inhibit the growth of cells that express EGFR. Such functional equivalents include, for example, chimerized, humanized, and single chain antibodies as well as fragments thereof.

Functional equivalents of antibodies also include polypeptides with amino
20 acid sequences substantially the same as the amino acid sequence of the variable or hypervariable regions of the antibodies. An amino acid sequence that is substantially the same as another sequence, but that differs from the other sequence by means of one or more substitutions, additions, and/or deletions, is considered to be an equivalent sequence. Preferably, less than 50%, more preferably less than 25%, and
25 still more preferably less than 10%, of the number of amino acid residues in a sequence are substituted for, added to, or deleted from the protein.

The functional equivalent of an antibody is preferably a chimerized or humanized antibody. A chimerized antibody comprises the variable region of a non-human antibody and the constant region of a human antibody. A humanized antibody
30 comprises the hypervariable region (CDRs) of a non-human antibody. The variable region other than the hypervariable region, e.g., the framework variable region, and the constant region of a humanized antibody are those of a human antibody.

Suitable variable and hypervariable regions of non-human antibodies may be derived from antibodies produced by any non-human mammal in which monoclonal antibodies are made. Suitable examples of mammals other than humans include, for example, rabbits, rats, mice, horses, goats, or primates.

5 Functional equivalents further include fragments of antibodies that have binding characteristics that are the same as, or are comparable to, those of the whole antibody. Suitable fragments of the antibody include any fragment that comprises a sufficient portion of the hypervariable (i.e., complementarity determining) region to bind specifically, and with sufficient affinity, to EGFR tyrosine kinase to inhibit
10 growth of cells that express such receptors.

Such fragments may, for example, contain one or both Fab fragments or the F(ab')₂ fragment. Preferably, the antibody fragments contain all six complementarity determining regions of the whole antibody, although functional fragments containing fewer than all of such regions, such as three, four, or five CDRs, are also included.

15 In one aspect, the fragments are single chain antibodies, or Fv fragments. Single chain antibodies are polypeptides that comprise at least the variable region of the heavy chain of the antibody linked to the variable region of the light chain, with or without an interconnecting linker. Thus, Fv fragment comprises the entire antibody combining site. These chains may be produced in bacteria or in eukaryotic cells.

20 The antibodies and functional equivalents may be members of any class of immunoglobulins, such as IgG, IgM, IgA, IgD, or IgE, and the subclasses thereof. In one aspect, the antibodies are members of the IgG1 subclass. The functional equivalents may also be equivalents of combinations of any of the above classes and subclasses.

25 In one aspect, EGFR antibodies can be selected from chimerized, humanized, fully human, and single chain antibodies derived from the murine antibody 225 described in U.S. Patent No. 4,943,533 to Mendelsohn et al. In one aspect, the 225 derived antibodies have the following hypervariable (CDR) regions of the light and heavy chain, wherein the amino acid sequences are indicated below the nucleotide
30 sequences:

HEAVY CHAIN HYPERVARIABLE REGIONS (VH):

CDR1

AACTATGGTGTACAC (SEQ ID NO: 179)

N Y G V H (SEQ ID NO: 180)

CDR2

5 GTGATATGGAGTGGTGGAAACACAGACTATAATACACCTTTCACATCC
(SEQ ID NO: 181)

V I W S G G N T D Y N T P F T S (SEQ ID NO: 182)

CDR3

GCCCTCACCTACTATGATTACGAGTTTGCTTAC (SEQ ID NO: 183)

10 A L T Y Y D Y E F A Y (SEQ ID NO: 184)

LIGHT CHAIN HYPERVARIABLE REGIONS (VL):

CDR1

AGGGCCAGTCAGAGTATTGGCACAAACATACAC (SEQ ID NO: 185)

15 R A S Q S I G T N I H (SEQ ID NO: 186)

CDR2

GCTTCTGAGTCTATCTCT (SEQ ID NO: 187)

A S E S I S (SEQ ID NO: 188)

CDR3

20 CAACAAAATAATAACTGGCCAACCACG (SEQ ID NO: 189)

Q Q N N N W P T T (SEQ ID NO: 190)

In another aspect, the EGFR antibody can be selected from the antibodies described in U.S. Patent No. 6,235,883 to Jakobovits et al., U.S. Patent No. 5,558,864 to Bendi et al., and U.S. Patent No. 5,891,996 to Mateo de Acosta del Rio et al.

25

In addition to the biological molecules discussed above, the EGFR modulators useful in the invention may also be small molecules. Any molecule that is not a biological molecule is considered herein to be a small molecule. Some examples of small molecules include organic compounds, organometallic compounds, salts of organic and organometallic compounds, saccharides, amino acids, and nucleotides.

30

Small molecules further include molecules that would otherwise be considered biological molecules, except their molecular weight is not greater than 450. Thus,

small molecules may be lipids, oligosaccharides, oligopeptides, and oligonucleotides and their derivatives, having a molecular weight of 450 or less.

It is emphasized that small molecules can have any molecular weight. They are merely called small molecules because they typically have molecular weights less than 450. Small molecules include compounds that are found in nature as well as synthetic compounds. In one embodiment, the EGFR modulator is a small molecule that inhibits the growth of tumor cells that express EGFR. In another embodiment, the EGFR modulator is a small molecule that inhibits the growth of refractory tumor cells that express EGFR.

Numerous small molecules have been described as being useful to inhibit EGFR. For example, U.S. Patent No. 5,656,655 to Spada et al. discloses styryl substituted heteroaryl compounds that inhibit EGFR. The heteroaryl group is a monocyclic ring with one or two heteroatoms, or a bicyclic ring with 1 to about 4 heteroatoms, the compound being optionally substituted or polysubstituted.

U.S. Patent No. 5,646,153 to Spada et al. discloses bis mono and/or bicyclic aryl heteroaryl, carbocyclic, and heterocarbocyclic compounds that inhibit EGFR.

U.S. Patent No. 5,679,683 to Bridges et al. discloses tricyclic pyrimidine compounds that inhibit the EGFR. The compounds are fused heterocyclic pyrimidine derivatives described at column 3, line 35 to column 5, line 6.

U.S. Patent No. 5,616,582 to Barker discloses quinazoline derivatives that have receptor tyrosine kinase inhibitory activity.

Fry et al., Science 265, 1093-1095 (1994) in Figure 1 discloses a compound having a structure that inhibits EGFR.

Osharov et al. disclose tyrphostins that inhibit EGFR/HER1 and HER 2, particularly those in Tables I, II, III, and IV.

U.S. Patent No. 5,196,446 to Levitzki et al. discloses heteroarylethenediyl or heteroarylethendeiylaryl compounds that inhibit EGFR, particularly from column 2, line 42 to column 3, line 40.

Panek et al., Journal of Pharmacology and Experimental Therapeutics 283, 1433-1444 (1997) discloses a compound identified as PD166285 that inhibits the EGFR, PDGFR, and FGFR families of receptors. PD166285 is identified as 6-(2,6-

dichlorophenyl)-2-(4-(2-diethylaminoethoxy)phenylamino)-8-methyl-8H-pyrido(2,3-d)pyrimidin-7-one having the structure shown in Figure 1 on page 1436.

BIOMARKERS AND BIOMARKER SETS

5 The invention includes individual biomarkers and biomarker sets having both diagnostic and prognostic value in disease areas in which signaling through EGFR or the EGFR pathway is of importance, e.g., in cancers or tumors, in immunological disorders, conditions or dysfunction, or in disease states in which cell signaling and/or cellular proliferation controls are abnormal or aberrant. The biomarker sets comprise
10 a plurality of biomarkers such as, for example, a plurality of the biomarkers provided in Table 4 below, that highly correlate with resistance or sensitivity to one or more EGFR modulators.

 The biomarker sets of the invention enable one to predict or reasonably foretell the likely effect of one or more EGFR modulators in different biological
15 systems or for cellular responses. The biomarker sets can be used in *in vitro* assays of EGFR modulator response by test cells to predict *in vivo* outcome. In accordance with the invention, the various biomarker sets described herein, or the combination of these biomarker sets with other biomarkers or markers, can be used, for example, to predict how patients with cancer might respond to therapeutic intervention with one or
20 more EGFR modulators.

 A biomarker set of cellular gene expression patterns correlating with sensitivity or resistance of cells following exposure of the cells to one or more EGFR modulators provides a useful tool for screening one or tumor samples before treatment with the EGFR modulator. The screening allows a prediction of cells of a tumor
25 sample exposed to one or more EGFR modulators, based on the expression results of the biomarker set, as to whether or not the tumor, and hence a patient harboring the tumor, will or will not respond to treatment with the EGFR modulator.

 The biomarker or biomarker set can also be used as described herein for monitoring the progress of disease treatment or therapy in those patients undergoing
30 treatment for a disease involving an EGFR modulator.

 The biomarkers serve as targets for the development of therapies for disease treatment. Such targets may be particularly applicable to treatment of breast disease,

such as breast cancers or tumors. Indeed, because these biomarkers are differentially expressed in sensitive and resistant cells, their expression patterns are correlated with relative intrinsic sensitivity of cells to treatment with EGFR modulators.

Accordingly, the biomarkers highly expressed in resistant cells may serve as targets
5 for the development of new therapies for the tumors which are resistant to EGFR modulators, particularly EGFR inhibitors.

MICROARRAYS

The invention also includes specialized microarrays, e.g., oligonucleotide
10 microarrays or cDNA microarrays, comprising one or more biomarkers, showing expression profiles that correlate with either sensitivity or resistance to one or more EGFR modulators. Such microarrays can be employed in *in vitro* assays for assessing the expression level of the biomarkers in the test cells from tumor biopsies, and determining whether these test cells are likely to be resistant or sensitive to EGFR
15 modulators. For example, a specialized microarray can be prepared using all the biomarkers, or subsets thereof, as described herein and shown in Table 4. Cells from a tissue or organ biopsy can be isolated and exposed to one or more of the EGFR modulators. Following application of nucleic acids isolated from both untreated and treated cells to one or more of the specialized microarrays, the pattern of gene
20 expression of the tested cells can be determined and compared with that of the biomarker pattern from the control panel of cells used to create the biomarker set on the microarray. Based upon the gene expression pattern results from the cells that underwent testing, it can be determined if the cells show a resistant or a sensitive profile of gene expression. Whether or not the tested cells from a tissue or organ
25 biopsy will respond to one or more of the EGFR modulators and the course of treatment or therapy can then be determined or evaluated based on the information gleaned from the results of the specialized microarray analysis.

ANTIBODIES

30 The invention also includes antibodies, including polyclonal or monoclonal, directed against one or more of the polypeptide biomarkers. Such antibodies can be used in a variety of ways, for example, to purify, detect, and target the biomarkers of

the invention, including both *in vitro* and *in vivo* diagnostic, detection, screening, and/or therapeutic methods.

KITS

5 The invention also includes kits for determining or predicting whether a patient would be susceptible or resistant to a treatment that comprises one or more EGFR modulators. The patient may have a cancer or tumor such as, for example, a breast cancer or tumor. Such kits would be useful in a clinical setting for use in testing a patient's biopsied tumor or cancer samples, for example, to determine or
10 predict if the patient's tumor or cancer will be resistant or sensitive to a given treatment or therapy with an EGFR modulator. The kit comprises a suitable container that comprises: one or more microarrays, e.g., oligonucleotide microarrays or cDNA microarrays, that comprise those biomarkers that correlate with resistance and sensitivity to EGFR modulators, particularly EGFR inhibitors; one or more EGFR
15 modulators for use in testing cells from patient tissue specimens or patient samples; and instructions for use. In addition, kits contemplated by the invention can further include, for example, reagents or materials for monitoring the expression of biomarkers of the invention at the level of mRNA or protein, using other techniques and systems practiced in the art such as, for example, RT-PCR assays, which employ
20 primers designed on the basis of one or more of the biomarkers described herein, immunoassays, such as enzyme linked immunosorbent assays (ELISAs), immunoblotting, e.g., Western blots, or *in situ* hybridization, and the like, as further described herein.

25 APPLICATION OF BIOMARKERS AND BIOMARKER SETS

 The biomarkers and biomarker sets may be used in different applications. Biomarker sets can be built from any combination of biomarkers listed in Table 4 to make predictions about the likely effect of any EGFR modulator in different biological systems. The various biomarkers and biomarker sets described herein can
30 be used, for example, as diagnostic or prognostic indicators in disease management, to predict how patients with cancer might respond to therapeutic intervention with compounds that modulate the EGFR, and to predict how patients might respond to

therapeutic intervention that modulates signaling through the entire EGFR regulatory pathway.

While the data described herein were generated in cell lines that are routinely used to screen and identify compounds that have potential utility for cancer therapy, the biomarkers have both diagnostic and prognostic value in other diseases areas in which signaling through EGFR or the EGFR pathway is of importance, e.g., in immunology, or in cancers or tumors in which cell signaling and/or proliferation controls have gone awry.

In the examples described below, the sensitivity and resistance classifications in the twenty two colon cell lines were similar for the two EGFR modulators tested. Therefore, the biomarkers of the invention are expected to have both diagnostic and prognostic value for other compounds that modulate EGFR or the EGFR signaling pathways.

Those having skill in the pertinent art will appreciate that the EGFR signaling pathway is used and functional in cell types other than cell lines of colon tissue. Therefore, the described biomarkers are expected to have utility for predicting drug sensitivity or resistance to compounds that interact with or inhibit the EGFR activity in cells from other tissues or organs associated with a disease state, or cancers or tumors derived from other tissue types. Non-limiting examples of such cells, tissues and organs include breast, colon, lung, prostate, testes, ovaries, cervix, esophagus, pancreas, spleen, liver, kidney, stomach, lymphocytic and brain, thereby providing a broad and advantageous applicability to the biomarkers described herein. Cells for analysis can be obtained by conventional procedures as known in the art, for example, tissue biopsy, aspiration, sloughed cells, e.g., colonocytes, clinical or medical tissue or cell sampling procedures.

In accordance with the invention, cells from a patient tissue sample, e.g., a tumor or cancer biopsy, can be assayed to determine the expression pattern of one or more biomarkers prior to treatment with one or more EGFR modulators. Success or failure of a treatment can be determined based on the biomarker expression pattern of the cells from the test tissue (test cells), e.g., tumor or cancer biopsy, as being relatively similar or different from the expression pattern of a control set of the one or more biomarkers. Thus, if the test cells show a biomarker expression profile which

corresponds to that of the biomarkers in the control panel of cells which are sensitive to the EGFR modulator, it is highly likely or predicted that the individual's cancer or tumor will respond favorably to treatment with the EGFR modulator. By contrast, if the test cells show a biomarker expression pattern corresponding to that of the

5 biomarkers of the control panel of cells which are resistant to the EGFR modulator, it is highly likely or predicted that the individual's cancer or tumor will not respond to treatment with the EGFR modulator.

The invention also provides a method of monitoring the treatment of a patient having a disease treatable by one or more EGFR modulators. The isolated test cells

10 from the patient's tissue sample, e.g., a tumor biopsy or tumor sample, can be assayed to determine the expression pattern of one or more biomarkers before and after exposure to an EGFR modulator wherein, preferably, the EGFR modulator is an EGFR inhibitor. The resulting biomarker expression profile of the test cells before and after treatment is compared with that of one or more biomarkers as described and

15 shown herein to be highly expressed in the control panel of cells that are either resistant or sensitive to an EGFR modulator. Thus, if a patient's response is sensitive to treatment by an EGFR modulator, based on correlation of the expression profile of the one or biomarkers, the patient's treatment prognosis can be qualified as favorable and treatment can continue. Also, if, after treatment with an EGFR modulator, the

20 test cells don't show a change in the biomarker expression profile corresponding to the control panel of cells that are sensitive to the EGFR modulator, it can serve as an indicator that the current treatment should be modified, changed, or even discontinued. This monitoring process can indicate success or failure of a patient's treatment with an EGFR modulator and such monitoring processes can be repeated as

25 necessary or desired.

The biomarkers of the invention can be used to predict an outcome prior to having any knowledge about a biological system. Essentially, a biomarker can be considered to be a statistical tool. Biomarkers are useful primarily in predicting the phenotype that is used to classify the biological system. In an embodiment of the

30 invention, the goal of the prediction is to classify cancer cells as having an active or inactive EGFR pathway. Cancer cells with an inactive EGFR pathway can be considered resistant to treatment with an EGFR modulator. An inactive EGFR

pathway is defined herein as a non-significant expression of the EGFR or by a classification as “resistant” or “sensitive” based on the IC₅₀ value of each colon cell line to a compound (EGFR inhibitor compound BMS-461453) exemplified herein.

A number of the biomarker described herein are known to be regulated by EGFR, e.g., mucin 2 (J Biol Chem. 2002 Aug 30;277(35):32258-67). Another biomarker, betacellulin, is known to be an EGFR ligand (Biochem Biophys Res Commun. 2002 Jun 28;294(5):1040-6). A functional relationship of the top biomarkers to the EGFR is expected, since biomarkers that contribute to high biomarker accuracy are likely to play a functional role in the pathway that is being modulated. For example, Perception therapy (i.e., antibody that binds to the Her2 receptor and prevents function via internalization) is indicated when the Her2 gene is overexpressed. It is unlikely that a therapy will have any therapeutic effect if the target enzyme is not expressed.

However, although the complete function of all of the biomarkers are not currently known, some of the biomarkers are likely to be directly or indirectly involved in the EGFR signaling pathway. In addition, some of the biomarkers may function in the metabolic or other resistance pathways specific to the EGFR modulators tested. Notwithstanding, knowledge about the function of the biomarkers is not a requisite for determining the accuracy of a biomarker according to the practice of the invention.

DISCOVERY OF BIOMARKERS

An approach has been discovered in which biomarkers were identified whose expression patterns, in a subset of cell lines, correlated to and can be used as an *in vitro* marker of cellular response to treatment or therapy with one compound, or with a combination or series of compounds, that are known to inhibit or activate the function of a protein, enzyme, or molecule (e.g., a receptor) that is directly or indirectly involved in cell proliferation, cell responses to external stimuli, (such as ligand binding), or signal transduction, e.g., a receptor tyrosine kinase. Preferred are antagonists or inhibitors of the function of a given protein, e.g., a receptor tyrosine kinase.

Two analytical strategies were deployed to discover biomarkers useful for predicting the sensitivity or resistance of cancer cells to treatment with one or more EGFR modulators. FIG. 1 illustrates the EGFR biomarker identification and prioritization strategy. In one strategy, the mRNA expression level of EGFR was used to identify six colon cancer cell lines with, inferred from the mRNA expression level, no significant presence of the EGFR protein and hence no significant activity of the EGFR pathway (FIG. 2A). In subsequent analyses, biomarkers were identified that had no significant mRNA expression level in the six cell lines and no inferred presence of the EGFR protein. Further, it was required that these biomarkers would have a significant mRNA expression level in at least six other cell lines.

In a second strategy, an EGFR specific tyrosine kinase inhibitor compound was used to determine compound sensitivity in a panel of twenty two colon cancer cell lines following exposure of the cells to the compound. Some of the cell lines were determined to be resistant to treatment with the inhibitor compound, while others were determined to be sensitive to the inhibitor (FIG. 2B). A subset of the cell lines examined provided an expression pattern or profile of biomarkers that correlated to a response by the cells to the EGFR inhibitor compound as well as the absence of significant EGFR expression as thus could serve as biomarkers.

By combining the use of EGFR co-regulation studies in tumor cells with experimental studies in cultured cells as a model of *in vivo* effects, the invention advantageously focuses on cell-intrinsic properties that are exposed in cell culture to identify biomarkers that predict compound sensitivity and resistance. The discovery and identification of biomarkers in tumor cells and cell lines assayed *in vitro* can be used to predict responses to one or more EGFR modulators *in vivo* and, thus, can be extended to clinical situations in which the same biomarkers are used to predict patients' responses to one or more EGFR modulators and treatments comprising one or more EGFR modulators.

As described in the examples below, oligonucleotide microarrays were used to measure the expression levels of over 44,792 probe sets in a panel of thirty one untreated colon cancer cell lines for which the expression status of the EGFR and the drug sensitivity to EGFR inhibitor compounds was determined. This analysis was performed to determine whether the gene expression signatures of untreated cells

were sufficient for the prediction of sensitivity of the disease to inhibition of the EGFR by small molecule or biological molecule compounds. Through data analysis, biomarkers were identified whose expression levels were found to be highly counter-correlated with the status of the EGFR and correlated with the drug sensitivity. In addition, the treatment of cells with a small molecule EGFR inhibitor also provided gene expression signatures predictive of sensitivity to the compound.

The means of performing the gene expression and biomarker identification analyses embraced by the invention is described in further detail and without limitation below.

10

IC₅₀ Determination and Phenotype Classification Based on Sensitivity of Twenty-two Colon Cancer Cell lines to EGFR Inhibitor Compounds

Twenty two colon cell lines were treated with a small molecule EGFR inhibitor (BMS-461453) to determine the individual IC₅₀ value. The IC₅₀ for each cell line was assessed by MTS assays. The average IC₅₀ values along with standard deviations were calculated from two to five individual determinations for each cell line. As shown in FIG. 2B, a 4-fold variation in the IC₅₀ values was observed for the small molecule EGFR inhibitor among the 22 colon cancer cell lines. The IC₅₀ unit is μ M.

20

All cell lines with at least a 1.75 fold lower IC₅₀ than the most resistant cell lines were considered to be sensitive to treatment with the small molecule EGFR inhibitor. FIG. 2B represents the resistance/sensitivity classifications of the twenty-two colon cell lines to the small molecule EGFR inhibitor. Five cell lines were classified as sensitive and seventeen cell lines as resistant.

25

Description of the Strategy for Identifying Biomarkers

Biomarkers were discovered based on two criteria: (i) the correlation of their mRNA expression level to the expression of EGFR in cell lines with insignificant EGFR expression and (ii) the correlation of the IC₅₀ values for the small molecule EGFR inhibitor BMS-461453 with gene expression levels.

30

For each of these two biomarker selection strategies, two independent "discovery" probe set lists were established by using statistical filters with different

stringency levels to identify genes whose expression correlated with either EGFR status or IC₅₀ value. These statistical methods are described below and resulted in four discovery probe set lists: EGFR-A and EGFR-B (correlation with no significant EGFR expression) and IC-50-A, IC-50-B (correlation with IC₅₀ expression), the A-
5 lists containing probe sets selected by more stringent conditions. To then establish two biomarker probe set lists, probe sets that appeared in both EGFR-A and IC-50 B were selected (Biomarker Probe Set List A, Table 2) and probe sets that appeared in both EGFR-B and IC-50-A were selected (Biomarker Probe Set List B, Table 3).

10 Identifying Genes that Significantly Correlate with EGFR status classification

RT-PCR expression data for EGFR were obtained from thirty one colon cancer cell lines and six cell lines with a significantly lower expression level of EGFR compared to the other cell lines were identified as described in Example 1 below. (FIG. 2A). Expression profiling data of 44,792 probe sets represented on the HG-
15 U133 array set for all thirty one untreated colon cancer cell lines were obtained and analyzed for the identification of probe sets which would be correlated with the above described six cell lines with no significant mRNA expression of EGFR. For the discovery probe set list EGFR-A, all probe sets which were judged to be absent by the Affymetrix Mas 5.0 software in six of the six colon cancer cell lines with significantly
20 lower expression of EGFR were identified. Second, it was required that these probe sets would be judged to be present in at least six cell lines of the twenty five cell lines classified as having significant mRNA expression of the EGFR. This analytical strategy resulted in the identification of 280 probe sets that could be analyzed in comparison to the discovery probe set list IC-50-B.

25 The discovery probe set list EGFR-B was generated by selecting all probe sets which were judged to be absent by the Affymetrix Mas 5.0 software in five of the six colon cancer cell lines with significantly lower expression of EGFR and which would be present in at least six cell lines of the twenty five cell lines classified as having significant mRNA expression of the EGFR. Discovery probe set list EGR-B contains
30 1,852 probe sets (U133A: 876; U133B: 976).

Identifying Genes that Significantly Correlate with Drug Resistance/Sensitivity Classification

Expression profiling data of 44,792 probe sets represented on the HG-U133 array set for twenty two untreated colon cell lines were obtained and preprocessed as described in Example 1 below. These data were analyzed using the Student's TTEST to identify genes whose expression patterns were strongly correlated with the drug resistance/sensitivity classification. Table 1 provides the resistance/sensitivity phenotype classification of the twenty two colon cell lines for the EGFR antagonist BMS-461453 based on the IC_{50} results. The mean IC_{50} values along with standard deviations (SD) were calculated from 2 to 5 individual determinations for each cell line as shown. The mean IC_{50} across the twenty two colon cell lines for BMS-461453 was calculated and used to normalize the IC_{50} data for each cell line. All cell lines with at least a 1.75 fold lower IC_{50} than the most resistant cell lines were considered to be sensitive to treatment with BMS-461453. The cell lines designated with an asterisk are defined as being sensitive to the drug treatment.

TABLE 1 - Resistance/Sensitivity Phenotype Classification of Twenty Two Colon Cell Lines

Cell lines	IC ₅₀ (μM)	SD
CCD_33C0*	2	1.28
LOVO*	2.3	2.28
LS174T*	3.5	1.93
Caco2*	5.5	3.97
SW403*	5.7	4.94
CCD18Co	7.1	3.84
SW837	7.2	3.30
Sk-Co-1	9	2.02
MIP	9.7	0.52
SW1417	10	0.00
HT-29	10	0.00
T84	10	0.00
CX-1	10	0.00
Colo-205	10	0.00
Colo-201	10	0.00
Colo320HSR	10	0.00
HCT8	10	0.00
Colo320DM	10	0.00
SW480	10	0.00
HCT116	10	0.00
SW620	10	0.00
HCT116S542	10	0.00

An “idealized expression pattern” corresponds to a gene that is uniformly high in one class (e.g., sensitive) and uniformly low in the other (e.g., resistant). Initially, a Student TTEST was performed in which a T value was obtained for each probe set.

- 5 Once a T value was generated, its corresponding confidence value (P) was found on a standard table of significance. The confidence value is a measure of the probability to observe a certain mean expression difference between two groups by chance alone and is obtained using the following formula:

$$T(g,c) = (X_1 - X_2) / (\text{var}_1/n_1 + \text{var}_2/n_2)^{1/2}$$

wherein,

T(g,c) represents the T value between expression for gene g and the sensitivity/resistance classification c;

5 X_1 represents mean gene expression level of samples in class 1;

X_2 represents mean gene expression level of samples in class 2;

var_1 represents variance of gene expression for samples in class 1;

var_2 represents variance of gene expression for samples in class 2;

n_1 represents number of samples in class 1;

10 n_2 represents number of samples in class 2; and

corresponding confidence value (P) for T values are obtained from a standard table of significance.

To generate discovery probe set list IC-50-B, a confidence value of 0.05 or lower was used as the cut off for probe sets to be included in the list. Discovery probe
15 set list IC-50-B contains 5,050 probe sets (U133A: 2,498; U133B: 2,552).

Discovery probe set list IC-50-A was generated using the Pearson correlation coefficient (a dimensionless index that ranges from -1.0 to 1.0). This value was calculated by treating the IC₅₀ data as continuous variables and by utilizing a linear regression model to correlate gene expression levels with IC₅₀ values for twenty-two
20 colon cell lines. Probe sets with a correlation coefficient less than -0.5 were selected (p < 0.02), a total of 902 probe sets (U133A: 467; U133B: 435).

Finally, two separate biomarker probe set lists were generated, biomarker probe set lists A and B, by identifying probe sets which were present in EGFR-A and IC-50-B (Biomarker Probe Set List A) (Table 2) or were present in EGFR-B and IC-
25 50-A (Biomarker Probe Set List B) (Table 3).

The biomarker probe set list A (Table 2) contains a total of 74 probe sets (U133A: 43; U133B: 31) and provides the polynucleotides identified to be biomarkers of EGFR antagonist sensitivity employing strategy A. With strategy A, polynucleotides were required to satisfy a stringent criteria for EGFR status
30 coregulation and a less stringent condition for correlation to IC₅₀ values. Namely, the polynucleotides had to be called absent by the Affymetrix software in six out of the

six cell lines with lowest expression of EGFR and be differentially expressed in the sensitive and resistance cell lines with a P value equal to or less than 0.05.

TABLE 2 - Biomarker Probe Set List A

Unigene Title	Affymetrix Description	Affymetrix probe set
hemoglobin, alpha 1	gb:BC005931.1 /DEF=Homo sapiens, hemoglobin, alpha 2, clone MGC:14541, mRNA, complete cds. /FEA=mRNA /PROD=hemoglobin, alpha 2 /DB_XREF=gi:13543547 /FL=gb:BC005931.1	211745_x_at
dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)	gb:M80536.1 /DEF=H.sapiens dipeptidyl peptidase IV (DPP4) mRNA, complete cds. /FEA=mRNA /GEN=DPP4 /PROD=dipeptidyl peptidase IV /DB_XREF=gi:181569 /UG=Hs.44926 dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2) /FL=gb:M80536.1 gb:NM_001935.1	203716_s_at
spondin 1, (f-spondin) extracellular matrix protein	Consensus includes gb:AI885290 /FEA=EST /DB_XREF=gi:5590454 /DB_XREF=est:wl92a04.x1 /CLONE=IMAGE:2432334 /UG=Hs.5378 spondin 1, (f-spondin) extracellular matrix protein	213994_s_at
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	gb:NM_005518.1 /DEF=Homo sapiens 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial) (HMGCS2), mRNA. /FEA=mRNA /GEN=HMGCS2 /PROD=3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2(mitochondrial) /DB_XREF=gi:5031750 /UG=Hs.59889 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial) /FL=gb:NM_005518.1	204607_at
mucin 2, intestinal/trachea 1	gb:NM_002457.1 /DEF=Homo sapiens mucin 2, intestinaltracheal (MUC2), mRNA. /FEA=mRNA /GEN=MUC2 /PROD=mucin 2, intestinaltracheal /DB_XREF=gi:4505284 /UG=Hs.315 mucin 2, intestinaltracheal /FL=gb:NM_002457.1 gb:L21998.1	204673_at
cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7)	gb:NM_000492.2 /DEF=Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA. /FEA=mRNA /GEN=CFTR /PROD=cystic fibrosis transmembrane conductanceregulator, ATP-binding cassette (sub-family C, member 7) /DB_XREF=gi:6995995	205043_at

	/UG=Hs.663 cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) /FL=gb:NM_000492.2	
CUG triplet repeat, RNA-binding protein 2	Consensus includes gb:N36839 /FEA=EST /DB_XREF=gi:1157981 /DB_XREF=est:yy35f07.s1 /CLONE=IMAGE:273253 /UG=Hs.211610 CUG triplet repeat, RNA-binding protein 2 /FL=gb:U69546.1 gb:AF036956.1 gb:AF090694.1 gb:NM_006561.1	202156_s_at
nuclear receptor subfamily 3, group C, member 2	gb:NM_000901.1 /DEF=Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA. /FEA=mRNA /GEN=NR3C2 /PROD=nuclear receptor subfamily 3, group C, member 2 /DB_XREF=gi:4505198 /UG=Hs.1790 nuclear receptor subfamily 3, group C, member 2 /FL=gb:M16801.1 gb:NM_000901.1	205259_at
cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7)	Consensus includes gb:W60595 /FEA=EST /DB_XREF=gi:1367354 /DB_XREF=est:zc91b04.s1 /CLONE=IMAGE:338479 /UG=Hs.663 cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7)	215702_s_at
cytochrome P450, subfamily IIJ (arachidonic acid epoxidase) polypeptide 2	gb:NM_000775.1 /DEF=Homo sapiens cytochrome P450, subfamily IIJ (arachidonic acid epoxidase) polypeptide 2 (CYP2J2), mRNA. /FEA=mRNA /GEN=CYP2J2 /PROD=cytochrome P450, subfamily IIJ (arachidonic acid epoxidase) polypeptide 2 /DB_XREF=gi:4503226 /UG=Hs.152096 cytochrome P450, subfamily IIJ (arachidonic acid epoxidase) polypeptide 2 /FL=gb:U37143.1 gb:NM_000775.1	205073_at
cystatin S	gb:NM_001899.1 /DEF=Homo sapiens cystatin S (CST4), mRNA. /FEA=mRNA /GEN=CST4 /PROD=cystatin S /DB_XREF=gi:4503108 /UG=Hs.56319 cystatin S /FL=gb:NM_001899.1	206994_at
spondin 1, (f-spondin) extracellular matrix protein	Consensus includes gb:AI885290 /FEA=EST /DB_XREF=gi:5590454 /DB_XREF=est:w192a04.x1 /CLONE=IMAGE:2432334 /UG=Hs.5378 spondin 1, (f-spondin) extracellular matrix protein	213993_at
fibroblast growth factor receptor 2 (bacteria-expressed kinase, craniofacial dysostosis 1, Crouzon syndrome,	gb:NM_022969.1 /DEF=Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome,	203638_s_at

keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	Pfeiffer syndrome, Jackson-Weiss syndrome) (FGFR2), transcript variant 2, mRNA. /FEA=mRNA /GEN=FGFR2 /PROD=fibroblast growth factor receptor 2, isoform 2precursor /DB_XREF=gi:13186252 /UG=Hs.278581 fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome) /FL=gb:NM_022969.1 gb:M97193.1 gb:M80634.1	
mucin 3B	Consensus includes gb:AB038783.1 /DEF=Homo sapiens MUC3B mRNA for intestinal mucin, partial cds. /FEA=mRNA /GEN=MUC3B /PROD=intestinal mucin /DB_XREF=gi:9929917 /UG=Hs.129782 mucin 3A, intestinal	214898_x_at
AA	Consensus includes gb:AV728958 /FEA=EST /DB_XREF=gi:10838379 /DB_XREF=est:AV728958 /CLONE=HTCBYF04 /UG=Hs.150443 KIAA0320 protein	212703_at
CUG triplet repeat, RNA-binding protein 2	gb:NM_006561.1 /DEF=Homo sapiens CUG triplet repeat, RNA-binding protein 2 (CUGBP2), mRNA. /FEA=mRNA /GEN=CUGBP2 /PROD=CUG triplet repeat, RNA-binding protein 2 /DB_XREF=gi:5729815 /UG=Hs.211610 CUG triplet repeat, RNA-binding protein 2 /FL=gb:U69546.1 gb:AF036956.1 gb:AF090694.1 gb:NM_006561.1	202158_s_at
spondin 1, (f-spondin) extracellular matrix protein	gb:AB051390.1 /DEF=Homo sapiens mRNA for VSGPF-spondin, complete cds. /FEA=mRNA /PROD=VSGPF-spondin /DB_XREF=gi:11320819 /UG=Hs.5378 spondin 1, (f-spondin) extracellular matrix protein /FL=gb:AB051390.1	209437_s_at
mucin 3B	Consensus includes gb:AF113616 /DEF=Homo sapiens intestinal mucin 3 (MUC3) gene, partial cds /FEA=mRNA /DB_XREF=gi:6466800 /UG=Hs.129782 mucin 3A, intestinal	214676_x_at
EphA1	gb:NM_005232.1 /DEF=Homo sapiens EphA1 (EPHA1), mRNA. /FEA=mRNA /GEN=EPHA1 /PROD=EphA1 /DB_XREF=gi:4885208 /UG=Hs.89839 EphA1 /FL=gb:M18391.1 gb:NM_005232.1	205977_s_at
matrilin 3	gb:NM_002381.2 /DEF=Homo sapiens matrilin 3 (MATN3) precursor, mRNA. /FEA=mRNA /GEN=MATN3 /PROD=matrilin 3 precursor /DB_XREF=gi:13518040 /UG=Hs.278461	206091_at

	matrilin 3 /FL=gb:NM_002381.2	
bone morphogenetic protein 2	gb:NM_001200.1 /DEF=Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /FEA=mRNA /GEN=BMP2 /PROD=bone morphogenetic protein 2 precursor /DB_XREF=gi:4557368 /UG=Hs.73853 bone morphogenetic protein 2 /FL=gb:NM_001200.1	205290_s_at
interferon consensus sequence binding protein 1	Consensus includes gb:AI073984 /FEA=EST /DB_XREF=gi:3400628 /DB_XREF=est:oy66c05.x1 /CLONE=IMAGE:1670792 /UG=Hs.14453 interferon consensus sequence binding protein 1 /FL=gb:M91196.1 gb:NM_002163.1	204057_at
retinoic acid receptor responder (tazarotene induced) 1	Consensus includes gb:AI669229 /FEA=EST /DB_XREF=gi:4834003 /DB_XREF=est:wc13e06.x1 /CLONE=IMAGE:2315074 /UG=Hs.82547 retinoic acid receptor responder (tazarotene induced) 1	221872_at
cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7)	Consensus includes gb:W60595 /FEA=EST /DB_XREF=gi:1367354 /DB_XREF=est:zc91b04.s1 /CLONE=IMAGE:338479 /UG=Hs.663 cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7)	215703_at
fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	gb:M87771.1 /DEF=Human secreted fibroblast growth factor receptor (K-sam-III) mRNA, complete cds. /FEA=mRNA /GEN=K-sam-III /PROD=fibroblast growth factor receptor /DB_XREF=gi:186781 /UG=Hs.278581 fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome) /FL=gb:NM_022970.1 gb:M87771.1	208228_s_at
myosin, heavy polypeptide 13, skeletal muscle	gb:NM_003802.1 /DEF=Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA. /FEA=mRNA /GEN=MYH13 /PROD=myosin, heavy polypeptide 13, skeletal muscle /DB_XREF=gi:11321578 /UG=Hs.278488 myosin, heavy polypeptide 13, skeletal muscle /FL=gb:NM_003802.1	208208_at

	gb:AF111782.2	
ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]	Consensus includes gb:AW675655 /FEA=EST /DB_XREF=gi:7540890 /DB_XREF=est:ba52e01.x1 /CLONE=IMAGE:2900184 /UG=Hs.314158 ESTs	222354_at
hypothetical protein FLJ20174	gb:NM_017699.1 /DEF=Homo sapiens hypothetical protein FLJ20174 (FLJ20174), mRNA. /FEA=mRNA /GEN=FLJ20174 /PROD=hypothetical protein FLJ20174 /DB_XREF=gi:8923170 /UG=Hs.114556 hypothetical protein FLJ20174 /FL=gb:NM_017699.1	219734_at
PTPRF interacting protein, binding protein 2 (liprin beta 2)	Consensus includes gb:AI692180 /FEA=EST /DB_XREF=gi:4969520 /DB_XREF=est:wd37f06.x1 /CLONE=IMAGE:2330339 /UG=Hs.12953 PTPRF interacting protein, binding protein 2 (liprin beta 2)	212841_s_at
ribonuclease, RNase A family, 1 (pancreatic)	gb:NM_002933.1 /DEF=Homo sapiens ribonuclease, RNase A family, 1 (pancreatic) (RNASE1), mRNA. /FEA=mRNA /GEN=RNASE1 /PROD=ribonuclease, RNase A family, 1 (pancreatic) /DB_XREF=gi:4506546 /UG=Hs.78224 ribonuclease, RNase A family, 1 (pancreatic) /FL=gb:BC005324.1 gb:NM_002933.1 gb:D26129.1	201785_at
hairless (mouse) homolog	gb:NM_018411.1 /DEF=Homo sapiens hairless protein (putative single zinc finger transcription factor protein, responsible for autosomal recessive universal congenital alopecia, HR gene) (HSA277165), mRNA. /FEA=mRNA /GEN=HSA277165 /PROD=hairless protein /DB_XREF=gi:11036651 /UG=Hs.272367 hairless protein (putative single zinc finger transcription factor protein, responsible for autosomal recessive universal congenital alopecia, HR gene) /FL=gb:NM_018411.1	220163_s_at
nuclear receptor subfamily 5, group A, member 2	Consensus includes gb:AF228413.1 /DEF=Homo sapiens hepatocyte transcription factor mRNA, 3UTR. /FEA=mRNA /DB_XREF=gi:7677372 /UG=Hs.183123 nuclear receptor subfamily 5, group A, member 2 /FL=gb:U93553.1 gb:AB019246.1 gb:AF124247.1	210174_at
superoxide dismutase 3, extracellular	gb:NM_003102.1 /DEF=Homo sapiens superoxide dismutase 3, extracellular (SOD3), mRNA. /FEA=mRNA /GEN=SOD3 /PROD=superoxide dismutase 3, extracellular	205236_x_at

	/DB_XREF=gi:4507150 /UG=Hs.2420 superoxide dismutase 3, extracellular /FL=gb:J02947.1 gb:NM_003102.1	
zinc finger protein 137 (clone pHZ-30)	gb:NM_003438.1 /DEF=Homo sapiens zinc finger protein 137 (clone pHZ-30) (ZNF137), mRNA. /FEA=mRNA /GEN=ZNF137 /PROD=zinc finger protein 137 (clone pHZ-30) /DB_XREF=gi:4507988 /UG=Hs.151689 zinc finger protein 137 (clone pHZ-30) /FL=gb:NM_003438.1 gb:U09414.1	207394_at
Homo sapiens mRNA; cDNA DKFZp564D042 (from clone DKFZp564D042)	Consensus includes gb:AL049983.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564D042 (from clone DKFZp564D042). /FEA=mRNA /DB_XREF=gi:4884234 /UG=Hs.240136 Homo sapiens mRNA; cDNA DKFZp564D042 (from clone DKFZp564D042)	217288_at
Hermansky-Pudlak syndrome	Consensus includes gb:AL022313 /DEF=Human DNA sequence from clone RP5-1119A7 on chromosome 22q12.2-12.3 Contains the TXN2 gene for mitochondrial thioredoxin, a novel gene, the EIF3S7 gene for eukaryotic translation initiation factor 3 subunit 7 (zeta, 6667kD) (EIF3-P66), the gene f... /FEA=CDS_3 /DB_XREF=gi:4200326 /UG=Hs.272270 Human DNA sequence from clone RP5-1119A7 on chromosome 22q12.2-12.3 Contains the TXN2 gene for mitochondrial thioredoxin, a novel gene, the EIF3S7 gene for eukaryotic translation initiation factor 3 subunit 7 (zeta, 6667kD) (EIF3-P66), the gene for a nov	217354_s_at
peroxisomal trans 2-enoyl CoA reductase; putative short chain alcohol dehydrogenase	gb:NM_018441.1 /DEF=Homo sapiens peroxisomal trans 2-enoyl CoA reductase; putative short chain alcohol dehydrogenase (HSA250303), mRNA. /FEA=mRNA /GEN=HSA250303 /PROD=peroxisomal trans 2-enoyl CoA reductase;putative short chain alcohol dehydrogenase /DB_XREF=gi:8923751 /UG=Hs.281680 peroxisomal trans 2-enoyl CoA reductase; putative short chain alcohol dehydrogenase /FL=gb:NM_018441.1	221142_s_at
BTG family, member 2	gb:NM_006763.1 /DEF=Homo sapiens BTG family, member 2 (BTG2), mRNA. /FEA=mRNA /GEN=BTG2 /PROD=BTG family, member 2 /DB_XREF=gi:5802987 /UG=Hs.75462 BTG family, member 2 /FL=gb:U72649.1 gb:NM_006763.1	201236_s_at
phosducin	gb:M33478.1 /DEF=Human 33-kDa phototransducing protein mRNA, complete cds.	211496_s_at

	/FEA=mRNA /DB_XREF=gi:177186 /UG=Hs.550 phosducin /FL=gb:NM_022577.1 gb:M33478.1 gb:AF076465.1	
Rho GTPase activating protein 8	gb:NM_015366.1 /DEF=Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), mRNA. /FEA=mRNA /GEN=ARHGAP8 /PROD=Rho GTPase activating protein 8 /DB_XREF=gi:7656903 /UG=Hs.102336 Rho GTPase activating protein 8 /FL=gb:NM_015366.1	205980_s_at
Homo sapiens clone 24707 mRNA sequence	Consensus includes gb:AW593996 /FEA=EST /DB_XREF=gi:7281254 /DB_XREF=est:hg41g06.x1 /CLONE=IMAGE:2948218 /UG=Hs.124969 Homo sapiens clone 24707 mRNA sequence	213256_at
caspase 10, apoptosis-related cysteine protease	gb:NM_001230.1 /DEF=Homo sapiens caspase 10, apoptosis-related cysteine protease (CASP10), mRNA. /FEA=mRNA /GEN=CASP10 /PROD=caspase 10, apoptosis- related cysteine protease /DB_XREF=gi:4502568 /UG=Hs.5353 caspase 10, apoptosis-related cysteine protease /FL=gb:U60519.1 gb:NM_001230.1	205467_at
KIAA0690 protein	Consensus includes gb:AK000238.1 /DEF=Homo sapiens cDNA FLJ20231 fis, clone COLF5511, highly similar to AB014590 Homo sapiens mRNA for KIAA0690 protein. /FEA=mRNA /DB_XREF=gi:7020188 /UG=Hs.60103 KIAA0690 protein	216360_x_at
Homo sapiens, Similar to RIKEN cDNA 1810037C20 gene, clone MGC:21481 IMAGE:385206 2, mRNA, complete cds	Consensus includes gb:AW001287 /FEA=EST /DB_XREF=gi:5848203 /DB_XREF=est:wu27e06.x1 /CLONE=IMAGE:2521282 /UG=Hs.61265 ESTs, Weakly similar to G786_HUMAN PROTEIN GS3786 H.sapiens	227676_at
ESTs	Consensus includes gb:AA581439 /FEA=EST /DB_XREF=gi:2359211 /DB_XREF=est:nh13c10.s1 /CLONE=IMAGE:952242 /UG=Hs.152328 ESTs	244650_at
ESTs	Consensus includes gb:AI739241 /FEA=EST /DB_XREF=gi:5101222 /DB_XREF=est:wi14h02.x1 /CLONE=IMAGE:2390259 /UG=Hs.171480 ESTs	238984_at

hypothetical protein FLJ23045	Consensus includes gb:AB046810.1 /DEF=Homo sapiens mRNA for KIAA1590 protein, partial cds. /FEA=mRNA /GEN=KIAA1590 /PROD=KIAA1590 protein /DB_XREF=gi:10047254 /UG=Hs.101774 hypothetical protein FLJ23045	232083_at
regenerating gene type IV	gb:AY007243.1 /DEF=Homo sapiens regenerating gene type IV mRNA, complete cds. /FEA=mRNA /PROD=regenerating gene type IV /DB_XREF=gi:12621025 /UG=Hs.105484 Homo sapiens regenerating gene type IV mRNA, complete cds /FL=gb:AY007243.1	223447_at
ESTs	Consensus includes gb:AI139990 /FEA=EST /DB_XREF=gi:3647447 /DB_XREF=est:qa47d03.x1 /CLONE=IMAGE:1689893 /UG=Hs.134586 ESTs	231022_at
ESTs	Consensus includes gb:AI733801 /FEA=EST /DB_XREF=gi:5054914 /DB_XREF=est:qk39c04.x5 /CLONE=IMAGE:1871334 /UG=Hs.146186 ESTs	237923_at
hypothetical protein MGC20702	Consensus includes gb:AK002203.1 /DEF=Homo sapiens cDNA FLJ11341 fis, clone PLACE1010786. /FEA=mRNA /DB_XREF=gi:7023932 /UG=Hs.10260 Homo sapiens cDNA FLJ11341 fis, clone PLACE1010786	226992_at
ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]	Consensus includes gb:AI457984 /FEA=EST /DB_XREF=gi:4312002 /DB_XREF=est:tj66a04.x1 /CLONE=IMAGE:2146446 /UG=Hs.165900 ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! H.sapiens	243729_at
Homo sapiens cDNA: FLJ22063 fis, clone HEP10326	Consensus includes gb:T86159 /FEA=EST /DB_XREF=gi:714511 /DB_XREF=est:yd84h07.s1 /CLONE=IMAGE:114973 /UG=Hs.10450 Homo sapiens cDNA: FLJ22063 fis, clone HEP10326	227724_at
ESTs	Consensus includes gb:AI806131 /FEA=EST /DB_XREF=gi:5392697 /DB_XREF=est:wf06c06.x1 /CLONE=IMAGE:2349802 /UG=Hs.99376	231148_at

	ESTs	
anterior gradient 2 (Xenopus laevis) homolog	Consensus includes gb:AI922323 /FEA=EST /DB_XREF=gi:5658287 /DB_XREF=est:wn90h03.x1 /CLONE=IMAGE:2453141 /UG=Hs.293380 ESTs	228969_at
ESTs	Consensus includes gb:AI493909 /FEA=EST /DB_XREF=gi:4394912 /DB_XREF=est:qz94e02.x1 /CLONE=IMAGE:2042234 /UG=Hs.6131 ESTs	235562_at
hypothetical protein FLJ22233	Consensus includes gb:AI339568 /FEA=EST /DB_XREF=gi:4076495 /DB_XREF=est:qk67e10.x1 /CLONE=IMAGE:1874058 /UG=Hs.286194 hypothetical protein FLJ22233 /FL=gb:NM_024959.1	222727_s_at
GalNAc alpha-2, 6-sialyltransferase I, long form	Consensus includes gb:Y11339.2 /DEF=Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form. /FEA=mRNA /PROD=GalNAc alpha-2,6-sialyltransferase I /DB_XREF=gi:7576275 /UG=Hs.105352 GalNAc alpha-2, 6-sialyltransferase I, long form	227725_at
ESTs	Consensus includes gb:AI917390 /FEA=EST /DB_XREF=gi:5637245 /DB_XREF=est:ts79a05.x1 /CLONE=IMAGE:2237456 /UG=Hs.99415 ESTs	240964_at
Homo sapiens cDNA: FLJ22751 fis, clone KAIA0483, highly similar to AF016692 Homo sapiens small intestinal mucin (MUC3) mRNA	Consensus includes gb:AK026404.1 /DEF=Homo sapiens cDNA: FLJ22751 fis, clone KAIA0483, highly similar to AF016692 Homo sapiens small intestinal mucin (MUC3) mRNA. /FEA=mRNA /DB_XREF=gi:10439257 /UG=Hs.271819 Homo sapiens cDNA: FLJ22751 fis, clone KAIA0483, highly similar to AF016692 Homo sapiens small intestinal mucin (MUC3) mRNA	232321_at
Homo sapiens cDNA: FLJ23331 fis, clone HEP12664	Consensus includes gb:AK026984.1 /DEF=Homo sapiens cDNA: FLJ23331 fis, clone HEP12664. /FEA=mRNA /DB_XREF=gi:10439980 /UG=Hs.50742 Homo sapiens cDNA: FLJ23331 fis, clone HEP12664	229021_at
ESTs	Consensus includes gb:AA827649 /FEA=EST /DB_XREF=gi:2900090 /DB_XREF=est:od01a12.s1 /CLONE=IMAGE:1357918 /UG=Hs.105317 ESTs	235515_at
prostate cancer	Consensus includes gb:AA633076 /FEA=EST	226167_at

associated protein 7	/DB_XREF=gi:2556490 /DB_XREF=est:nq38a06.s1 /CLONE=IMAGE:1146130 /UG=Hs.27495 prostate cancer associated protein 7	
ESTs	Consensus includes gb:N37023 /FEA=EST /DB_XREF=gi:1158165 /DB_XREF=est:yy40d03.s1 /CLONE=IMAGE:273701 /UG=Hs.235883 ESTs	225407_at
ESTs, Weakly similar to I38588 reverse transcriptase homolog [H.sapiens]	Consensus includes gb:AI864053 /FEA=EST /DB_XREF=gi:5528160 /DB_XREF=est:wj55h10.x1 /CLONE=IMAGE:2406787 /UG=Hs.39972 ESTs, Weakly similar to I38588 reverse transcriptase homolog H.sapiens	235678_at
ESTs, Weakly similar to JX0331 laurate omega-hydroxylase [H.sapiens]	Consensus includes gb:AA557324 /FEA=EST /DB_XREF=gi:2327801 /DB_XREF=est:nl81a02.s1 /CLONE=IMAGE:1057034 /UG=Hs.26040 ESTs, Weakly similar to fatty acid omega-hydroxylase H.sapiens	227702_at
ESTs	Consensus includes gb:BF594323 /FEA=EST /DB_XREF=gi:11686647 /DB_XREF=est:7h79g07.x1 /CLONE=IMAGE:3322236 /UG=Hs.158989 ESTs	238103_at
ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]	Consensus includes gb:AI827789 /FEA=EST /DB_XREF=gi:5448449 /DB_XREF=est:wf33a07.x1 /CLONE=IMAGE:2357364 /UG=Hs.100686 ESTs, Weakly similar to JE0350 Anterior gradient-2 H.sapiens	228241_at
ESTs	Consensus includes gb:AI968097 /FEA=EST /DB_XREF=gi:5764915 /DB_XREF=est:wu13a12.x1 /CLONE=IMAGE:2516830 /UG=Hs.131360 ESTs	237835_at
ESTs	Consensus includes gb:H05025 /FEA=EST /DB_XREF=gi:868577 /DB_XREF=est:y174g12.s1 /CLONE=IMAGE:43864 /UG=Hs.323767 ESTs	241874_at
Homo sapiens, Similar to RIKEN cDNA 1110060O18 gene, clone MGC:17236 IMAGE:386413	Consensus includes gb:AA524690 /FEA=EST /DB_XREF=gi:2265618 /DB_XREF=est:ng38e07.s1 /CLONE=IMAGE:937092 /UG=Hs.294143 ESTs, Weakly similar to predicted using Genefinder C.elegans	226168_at

7, mRNA, complete cds		
ESTs	Consensus includes gb:AI300126 /FEA=EST /DB_XREF=gi:3959472 /DB_XREF=est:qn54f02.x1 /CLONE=IMAGE:1902075 /UG=Hs.257858 ESTs	240830_at
Homo sapiens cDNA FLJ13137 fis, clone NT2RP3003150	Consensus includes gb:AA129774 /FEA=EST /DB_XREF=gi:1690185 /DB_XREF=est:z116h09.s1 /CLONE=IMAGE:502145 /UG=Hs.288905 Homo sapiens cDNA FLJ13137 fis, clone NT2RP3003150	227019_at
ESTs	Consensus includes gb:AW024656 /FEA=EST /DB_XREF=gi:5878186 /DB_XREF=est:wu78h05.x1 /CLONE=IMAGE:2526201 /UG=Hs.233382 ESTs, Moderately similar to AF119917 62 PRO2822 H.sapiens	242358_at

The biomarker probe set list B (Table 3) contains 95 probe sets (U133A: 47; U133B 48). The biomarker probe set list B contains polynucleotides identified to be biomarkers of EGFR antagonist sensitivity employing strategy B. In strategy B,

5 polynucleotides were required to satisfy a stringent criteria for correlation to IC₅₀ values and a less stringent condition for EGFR status coregulation. Namely, the polynucleotides had to have a Pearsons correlation of -0.5 or less with respect to IC₅₀ and be called absent by the Affymetrix software in 5 out of the 6 cell lines with lowest expression of EGFR.

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TABLE 3 - Biomarker Probe Set List B

Unigene Title	Affymetrix Description	Affymetrix probe set
dopa decarboxylase (aromatic L- amino acid decarboxylase)	Consensus includes gb:AW772056 /FEA=EST /DB_XREF=gi:7704118 /DB_XREF=est:hn64g06.x1 /CLONE=IMAGE:3032698 /UG=Hs.150403 dopa decarboxylase (aromatic L-amino acid decarboxylase)	214347_s_at
cystic fibrosis transmembrane conductance regulator, ATP- binding cassette	gb:NM_000492.2 /DEF=Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA. /FEA=mRNA /GEN=CFTR /PROD=cystic fibrosis transmembrane	205043_at

(sub-family C, member 7)	conductanceregulator, ATP-binding cassette (sub-family C, member 7) /DB_XREF=gi:6995995 /UG=Hs.663 cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) /FL=gb:NM_000492.2	
carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	gb:BC005008.1 /DEF=Homo sapiens, carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen), clone MGC:10467, mRNA, complete cds. /FEA=mRNA /PROD=carcinoembryonic antigen-related cell adhesionmolecule 6 (non-specific cross reacting antigen) /DB_XREF=gi:13477106 /UG=Hs.73848 carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) /FL=gb:BC005008.1 gb:M18216.1 gb:M29541.1 gb:NM_002483.1	203757_s_at
hypothetical protein FLJ20075	gb:NM_017655.1 /DEF=Homo sapiens hypothetical protein FLJ20075 (FLJ20075), mRNA. /FEA=mRNA /GEN=FLJ20075 /PROD=hypothetical protein FLJ20075 /DB_XREF=gi:8923083 /UG=Hs.205058 hypothetical protein FLJ20075 /FL=gb:NM_017655.1	219970_at
ATPase, Class V, type 10B	Consensus includes gb:AW006935 /FEA=EST /DB_XREF=gi:5855713 /DB_XREF=est:wt08b11.x1 /CLONE=IMAGE:2506845 /UG=Hs.109358 ATPase, Class V, type 10B	214070_s_at
cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7)	Consensus includes gb:W60595 /FEA=EST /DB_XREF=gi:1367354 /DB_XREF=est:zc91b04.s1 /CLONE=IMAGE:338479 /UG=Hs.663 cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7)	215702_s_at
HERV-H LTR-associating 2	gb:NM_007072.1 /DEF=Homo sapiens HERV-H LTR-associating 2 (HHLA2), mRNA. /FEA=mRNA /GEN=HHLA2 /PROD=HERV-H LTR-associating 2 /DB_XREF=gi:5901963 /UG=Hs.252351 HERV-H LTR-associating 2 /FL=gb:AF126162.1 gb:NM_007072.1	220812_s_at
AA	Consensus includes gb:AV728958 /FEA=EST /DB_XREF=gi:10838379 /DB_XREF=est:AV728958 /CLONE=HTCBYF04 /UG=Hs.150443 KIAA0320 protein	212703_at

hemoglobin, alpha 2	Consensus includes gb:T50399 /FEA=EST /DB_XREF=gi:652259 /DB_XREF=est:yb30b11.s1 /CLONE=IMAGE:72669 /UG=Hs.251577 hemoglobin, alpha 1	214414_x_at
spondin 1, (f- spondin) extracellular matrix protein	Consensus includes gb:AI885290 /FEA=EST /DB_XREF=gi:5590454 /DB_XREF=est:wl92a04.x1 /CLONE=IMAGE:2432334 /UG=Hs.5378 spondin 1, (f-spondin) extracellular matrix protein	213993_at
hemoglobin, alpha 1	gb:BC005931.1 /DEF=Homo sapiens, hemoglobin, alpha 2, clone MGC:14541, mRNA, complete cds. /FEA=mRNA /PROD=hemoglobin, alpha 2 /DB_XREF=gi:13543547 /FL=gb:BC005931.1	211745_x_at
serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5	gb:NM_002639.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5 (SERPINB5), mRNA. /FEA=mRNA /GEN=SERPINB5 /PROD=serine (or cysteine) proteinase inhibitor, cladeB (ovalbumin), member 5 /DB_XREF=gi:4505788 /UG=Hs.55279 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5 /FL=gb:NM_002639.1 gb:U04313.1	204855_at
3-hydroxy-3- methylglutaryl- Coenzyme A synthase 2 (mitochondrial)	gb:NM_005518.1 /DEF=Homo sapiens 3- hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial) (HMGCS2), mRNA. /FEA=mRNA /GEN=HMGCS2 /PROD=3- hydroxy-3-methylglutaryl-Coenzyme A synthase 2(mitochondrial) /DB_XREF=gi:5031750 /UG=Hs.59889 3-hydroxy-3-methylglutaryl- Coenzyme A synthase 2 (mitochondrial) /FL=gb:NM_005518.1	204607_at
anterior gradient 2 (Xenopus laevis) homolog	gb:AF088867.1 /DEF=Homo sapiens putative secreted protein XAG mRNA, complete cds. /FEA=mRNA /PROD=putative secreted protein XAG /DB_XREF=gi:6652811 /UG=Hs.91011 anterior gradient 2 (Xenopus laevis) homolog /FL=gb:AF007791.1 gb:AF038451.1 gb:NM_006408.1 gb:AF088867.1	209173_at
FXYP domain- containing ion transport regulator 3	gb:BC005238.1 /DEF=Homo sapiens, FXYP domain-containing ion transport regulator 3, clone MGC:12265, mRNA, complete cds. /FEA=mRNA /PROD=FXYP domain- containing ion transport regulator3 /DB_XREF=gi:13528881 /UG=Hs.301350 FXYP domain-containing ion transport regulator	202489_s_at

	3 /FL=gb:NM_005971.2 gb:BC005238.1	
dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)	gb:M80536.1 /DEF=H.sapiens dipeptidyl peptidase IV (DPP4) mRNA, complete cds. /FEA=mRNA /GEN=DPP4 /PROD=dipeptidyl peptidase IV /DB_XREF=gi:181569 /UG=Hs.44926 dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2) /FL=gb:M80536.1 gb:NM_001935.1	203716_s_at
cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7)	Consensus includes gb:W60595 /FEA=EST /DB_XREF=gi:1367354 /DB_XREF=est:zc91b04.s1 /CLONE=IMAGE:338479 /UG=Hs.663 cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7)	215703_at
EphA1	gb:NM_005232.1 /DEF=Homo sapiens EphA1 (EPHA1), mRNA. /FEA=mRNA /GEN=EPHA1 /PROD=EphA1 /DB_XREF=gi:4885208 /UG=Hs.89839 EphA1 /FL=gb:M18391.1 gb:NM_005232.1	205977_s_at
spondin 1, (f-spondin) extracellular matrix protein	Consensus includes gb:AI885290 /FEA=EST /DB_XREF=gi:5590454 /DB_XREF=est:wl92a04.x1 /CLONE=IMAGE:2432334 /UG=Hs.5378 spondin 1, (f-spondin) extracellular matrix protein	213994_s_at
CUG triplet repeat, RNA-binding protein 2	gb:NM_006561.1 /DEF=Homo sapiens CUG triplet repeat, RNA-binding protein 2 (CUGBP2), mRNA. /FEA=mRNA /GEN=CUGBP2 /PROD=CUG triplet repeat, RNA-binding protein 2 /DB_XREF=gi:5729815 /UG=Hs.211610 CUG triplet repeat, RNA-binding protein 2 /FL=gb:U69546.1 gb:AF036956.1 gb:AF090694.1 gb:NM_006561.1	202158_s_at
DKFZP434C091 protein	Consensus includes gb:AL080170.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434C091 (from clone DKFZp434C091); partial cds. /FEA=mRNA /GEN=DKFZp434C091 /PROD=hypothetical protein /DB_XREF=gi:5262639 /UG=Hs.51692 DKFZP434C091 protein	215047_at
mucin 3B	Consensus includes gb:AF113616 /DEF=Homo sapiens intestinal mucin 3 (MUC3) gene, partial cds /FEA=mRNA /DB_XREF=gi:6466800 /UG=Hs.129782 mucin 3A, intestinal	214676_x_at
potassium channel,	gb:U90065.1 /DEF=Human potassium channel KCNO1 mRNA, complete cds. /FEA=mRNA	204678_s_at

subfamily K, member 1 (TWIK-1)	/PROD=potassium channel KCNO1 /DB_XREF=gi:1916294 /UG=Hs.79351 potassium channel, subfamily K, member 1 (TWIK-1) /FL=gb:U33632.1 gb:U90065.1 gb:U76996.1 gb:NM_002245.1	
nuclear receptor subfamily 3, group C, member 2	gb:NM_000901.1 /DEF=Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA. /FEA=mRNA /GEN=NR3C2 /PROD=nuclear receptor subfamily 3, group C, member 2 /DB_XREF=gi:4505198 /UG=Hs.1790 nuclear receptor subfamily 3, group C, member 2 /FL=gb:M16801.1 gb:NM_000901.1	205259_at
BTG family, member 2	gb:NM_006763.1 /DEF=Homo sapiens BTG family, member 2 (BTG2), mRNA. /FEA=mRNA /GEN=BTG2 /PROD=BTG family, member 2 /DB_XREF=gi:5802987 /UG=Hs.75462 BTG family, member 2 /FL=gb:U72649.1 gb:NM_006763.1	201236_s_at
G protein- coupled receptor 49	gb:AF062006.1 /DEF=Homo sapiens orphan G protein-coupled receptor HG38 mRNA, complete cds. /FEA=mRNA /PROD=orphan G protein-coupled receptor HG38 /DB_XREF=gi:3366801 /UG=Hs.285529 G protein-coupled receptor 49 /FL=gb:AF062006.1 gb:AF061444.1 gb:NM_003667.1	210393_at
hypothetical protein FLJ20048	gb:NM_017640.1 /DEF=Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA. /FEA=mRNA /GEN=FLJ20048 /PROD=hypothetical protein FLJ20048 /DB_XREF=gi:8923056 /UG=Hs.116470 hypothetical protein FLJ20048 /FL=gb:NM_017640.1	219573_at
cytochrome P450, subfamily IIJ (arachidonic acid epoxygenase) polypeptide 2	gb:NM_000775.1 /DEF=Homo sapiens cytochrome P450, subfamily IIJ (arachidonic acid epoxygenase) polypeptide 2 (CYP2J2), mRNA. /FEA=mRNA /GEN=CYP2J2 /PROD=cytochrome P450, subfamily IIJ (arachidonic acid epoxygenase) polypeptide 2 /DB_XREF=gi:4503226 /UG=Hs.152096 cytochrome P450, subfamily IIJ (arachidonic acid epoxygenase) polypeptide 2 /FL=gb:U37143.1 gb:NM_000775.1	205073_at
brain-specific protein p25 alpha	gb:NM_007030.1 /DEF=Homo sapiens brain- specific protein p25 alpha (p25), mRNA. /FEA=mRNA /GEN=p25 /PROD=brain-specific protein p25 alpha /DB_XREF=gi:5902017 /UG=Hs.29353 brain-specific protein p25 alpha	206179_s_at

	/FL=gb:AB017016.1 gb:NM_007030.1	
mucin 2, intestinal/trachea 1	gb:NM_002457.1 /DEF=Homo sapiens mucin 2, intestinaltracheal (MUC2), mRNA. /FEA=mRNA /GEN=MUC2 /PROD=mucin 2, intestinaltracheal /DB_XREF=gi:4505284 /UG=Hs.315 mucin 2, intestinaltracheal /FL=gb:NM_002457.1 gb:L21998.1	204673_at
hypothetical protein FLJ20174	gb:NM_017699.1 /DEF=Homo sapiens hypothetical protein FLJ20174 (FLJ20174), mRNA. /FEA=mRNA /GEN=FLJ20174 /PROD=hypothetical protein FLJ20174 /DB_XREF=gi:8923170 /UG=Hs.114556 hypothetical protein FLJ20174 /FL=gb:NM_017699.1	219734_at
metastasis- associated 1-like 1	gb:NM_004739.1 /DEF=Homo sapiens metastasis-associated 1-like 1 (MTA1L1), mRNA. /FEA=mRNA /GEN=MTA1L1 /PROD=metastasis-associated 1-like 1 /DB_XREF=gi:4758739 /UG=Hs.173043 metastasis-associated 1-like 1 /FL=gb:AB016591.1 gb:NM_004739.1 gb:AF295807.1	203444_s_at
bone morphogenetic protein 2	gb:NM_001200.1 /DEF=Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /FEA=mRNA /GEN=BMP2 /PROD=bone morphogenetic protein 2 precursor /DB_XREF=gi:4557368 /UG=Hs.73853 bone morphogenetic protein 2 /FL=gb:NM_001200.1	205290_s_at
heparanase	gb:NM_006665.1 /DEF=Homo sapiens heparanase (HPSE), mRNA. /FEA=mRNA /GEN=HPSE /PROD=heparanase /DB_XREF=gi:5729872 /UG=Hs.44227 heparanase /FL=gb:AF165154.1 gb:AF152376.1 gb:NM_006665.1 gb:AF084467.1 gb:AF155510.1	219403_s_at
tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	gb:BC002794.1 /DEF=Homo sapiens, tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator), clone MGC:3753, mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator) /DB_XREF=gi:12803894 /UG=Hs.279899 tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator) /FL=gb:BC002794.1 gb:U70321.1 gb:U81232.1 gb:NM_003820.1 gb:AF153978.1	209354_at
CUG triplet repeat, RNA-	Consensus includes gb:N36839 /FEA=EST /DB_XREF=gi:1157981	202156_s_at

binding protein 2	/DB_XREF=est:yy35f07.s1 /CLONE=IMAGE:273253 /UG=Hs.211610 CUG triplet repeat, RNA-binding protein 2 /FL=gb:U69546.1 gb:AF036956.1 gb:AF090694.1 gb:NM_006561.1	
ESTs, Moderately similar to AF078844 1 hqp0376 protein [H.sapiens]	Consensus includes gb:R06655 /FEA=EST /DB_XREF=gi:757275 /DB_XREF=est:yf10e02.r1 /CLONE=IMAGE:126458 /UG=Hs.188518 ESTs, Moderately similar to AF078844 1 hqp0376 protein H.sapiens	217546_at
hairless (mouse) homolog	gb:NM_018411.1 /DEF=Homo sapiens hairless protein (putative single zinc finger transcription factor protein, responsible for autosomal recessive universal congenital alopecia, HR gene) (HSA277165), mRNA. /FEA=mRNA /GEN=HSA277165 /PROD=hairless protein /DB_XREF=gi:11036651 /UG=Hs.272367 hairless protein (putative single zinc finger transcription factor protein, responsible for autosomal recessive universal congenital alopecia, HR gene) /FL=gb:NM_018411.1	220163_s_at
branched chain aminotransferase 1, cytosolic	Consensus includes gb:NM_005504.1 /DEF=Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA. /FEA=CDS /GEN=BCAT1 /PROD=branched chain aminotransferase 1, cytosolic /DB_XREF=gi:5031606 /UG=Hs.157205 branched chain aminotransferase 1, cytosolic /FL=gb:U21551.1 gb:NM_005504.1	214452_at
pancreas- enriched phospholipase C	gb:NM_016341.1 /DEF=Homo sapiens pancreas-enriched phospholipase C (LOC51196), mRNA. /FEA=mRNA /GEN=LOC51196 /PROD=pancreas-enriched phospholipase C /DB_XREF=gi:7705940 /UG=Hs.6733 pancreas-enriched phospholipase C /FL=gb:AF190642.2 gb:AF117948.1 gb:NM_016341.1	205112_at
prostaglandin- endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	gb:NM_000963.1 /DEF=Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin GH synthase and cyclooxygenase) (PTGS2), mRNA. /FEA=mRNA /GEN=PTGS2 /PROD=prostaglandin-endoperoxide synthase 2(prostaglandin GH synthase and cyclooxygenase) /DB_XREF=gi:4506264 /UG=Hs.196384 prostaglandin-endoperoxide synthase 2 (prostaglandin GH synthase and	204748_at

	cyclooxygenase) /FL=gb:M90100.1 gb:L15326.1 gb:Nm_000963.1	
phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	gb:Nm_000314.1 /DEF=Homo sapiens phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN), mRNA. /FEA=mRNA /GEN=PTEN /PROD=phosphatase and tensin homolog (mutated in multiple advanced cancers 1) /DB_XREF=gi:4506248 /UG=Hs.10712 phosphatase and tensin homolog (mutated in multiple advanced cancers 1) /FL=gb:U92436.1 gb:U93051.1 gb:U96180.1 gb:Nm_000314.1	204054_at
retinoic acid receptor responder (tazarotene induced) 1	Consensus includes gb:AI669229 /FEA=EST /DB_XREF=gi:4834003 /DB_XREF=est:wc13e06.x1 /CLONE=IMAGE:2315074 /UG=Hs.82547 retinoic acid receptor responder (tazarotene induced) 1	221872_at
protease inhibitor 3, skin-derived (SKALP)	gb:Nm_002638.1 /DEF=Homo sapiens protease inhibitor 3, skin-derived (SKALP) (PI3), mRNA. /FEA=mRNA /GEN=PI3 /PROD=protease inhibitor 3, skin-derived (SKALP) /DB_XREF=gi:4505786 /UG=Hs.112341 protease inhibitor 3, skin-derived (SKALP) /FL=gb:Nm_002638.1	203691_at
zinc finger protein 137 (clone pHZ-30)	gb:Nm_003438.1 /DEF=Homo sapiens zinc finger protein 137 (clone pHZ-30) (ZNF137), mRNA. /FEA=mRNA /GEN=ZNF137 /PROD=zinc finger protein 137 (clone pHZ-30) /DB_XREF=gi:4507988 /UG=Hs.151689 zinc finger protein 137 (clone pHZ-30) /FL=gb:Nm_003438.1 gb:U09414.1	207394_at
myosin, light polypeptide 5, regulatory	gb:Nm_002477.1 /DEF=Homo sapiens myosin, light polypeptide 5, regulatory (MYL5), mRNA. /FEA=mRNA /GEN=MYL5 /PROD=myosin, light polypeptide 5, regulatory /DB_XREF=gi:4505304 /UG=Hs.170482 myosin, light polypeptide 5, regulatory /FL=gb:L03785.1 gb:Nm_002477.1	205145_s_at
tumor necrosis factor receptor superfamily, member 6	gb:Nm_000043.1 /DEF=Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), mRNA. /FEA=mRNA /GEN=TNFRSF6 /PROD=apoptosis (APO-1) antigen 1 /DB_XREF=gi:4507582 /UG=Hs.82359 tumor necrosis factor receptor superfamily, member 6 /FL=gb:M67454.1 gb:Nm_000043.1	204781_s_at
hypothetical	Consensus includes gb:AI339568 /FEA=EST	222727_s_at

protein FLJ22233	/DB_XREF=gi:4076495 /DB_XREF=est:qk67e10.x1 /CLONE=IMAGE:1874058 /UG=Hs.286194 hypothetical protein FLJ22233 /FL=gb:NM_024959.1	
regenerating gene type IV	gb:AY007243.1 /DEF=Homo sapiens regenerating gene type IV mRNA, complete cds. /FEA=mRNA /PROD=regenerating gene type IV /DB_XREF=gi:12621025 /UG=Hs.105484 Homo sapiens regenerating gene type IV mRNA, complete cds /FL=gb:AY007243.1	223447_at
Homo sapiens cDNA: FLJ21962 fis, clone HEP05564	Consensus includes gb:AK025615.1 /DEF=Homo sapiens cDNA: FLJ21962 fis, clone HEP05564. /FEA=mRNA /DB_XREF=gi:10438186 /UG=Hs.7567 Homo sapiens cDNA: FLJ21962 fis, clone HEP05564	225285_at
phosphoprotein associated with glycosphingolipi d-enriched microdomains	Consensus includes gb:AK000680.1 /DEF=Homo sapiens cDNA FLJ20673 fis, clone KAIA4464. /FEA=mRNA /DB_XREF=gi:7020924 /UG=Hs.266175 phosphoprotein associated with GEMs /FL=gb:AF240634.1 gb:NM_018440.1	225626_at
hypothetical protein FLJ20209	Consensus includes gb:BF111925 /FEA=EST /DB_XREF=gi:10941704 /DB_XREF=est:7138g05.x1 /CLONE=IMAGE:3523784 /UG=Hs.3685 hypothetical protein FLJ20209	226171_at
Homo sapiens mRNA for KIAA1190 protein, partial cds	Consensus includes gb:AA532640 /FEA=EST /DB_XREF=gi:2276894 /DB_XREF=est:nj17c04.s1 /CLONE=IMAGE:986598 /UG=Hs.206259 Homo sapiens mRNA for KIAA1190 protein, partial cds	226484_at
KIAA1543 protein	Consensus includes gb:AB040976.1 /DEF=Homo sapiens mRNA for KIAA1543 protein, partial cds. /FEA=mRNA /GEN=KIAA1543 /PROD=KIAA1543 protein /DB_XREF=gi:7959352 /UG=Hs.17686 KIAA1543 protein	226494_at
hypothetical protein FLJ23563	Consensus includes gb:AW138767 /FEA=EST /DB_XREF=gi:6143085 /DB_XREF=est:UI-H- BI1-aep-a-12-0-UI.s1 /CLONE=IMAGE:2719799 /UG=Hs.274256 hypothetical protein FLJ23563	227180_at
ESTs	Consensus includes gb:AW264333 /FEA=EST /DB_XREF=gi:6641075 /DB_XREF=est:xq98e01.x1	227320_at

	/CLONE=IMAGE:2758680 /UG=Hs.21835 ESTs	
ESTs	Consensus includes gb:BF589359 /FEA=EST /DB_XREF=gi:11681683 /DB_XREF=est:nab25d01.x1 /CLONE=IMAGE:3266737 /UG=Hs.13256 ESTs	227354_at
Homo sapiens, Similar to RIKEN cDNA 1810037C20 gene, clone MGC:21481 IMAGE:385206 2, mRNA, complete cds	Consensus includes gb:AW001287 /FEA=EST /DB_XREF=gi:5848203 /DB_XREF=est:wu27e06.x1 /CLONE=IMAGE:2521282 /UG=Hs.61265 ESTs, Weakly similar to G786_HUMAN PROTEIN GS3786 H.sapiens	227676_at
Homo sapiens cDNA: FLJ22063 fis, clone HEP10326	Consensus includes gb:T86159 /FEA=EST /DB_XREF=gi:714511 /DB_XREF=est:yd84h07.s1 /CLONE=IMAGE:114973 /UG=Hs.10450 Homo sapiens cDNA: FLJ22063 fis, clone HEP10326	227724_at
ESTs	Consensus includes gb:AI700341 /FEA=EST /DB_XREF=gi:4988241 /DB_XREF=est:wd06e10.x1 /CLONE=IMAGE:2327370 /UG=Hs.110406 ESTs	228653_at
ESTs	Consensus includes gb:BG494007 /FEA=EST /DB_XREF=gi:13455521 /DB_XREF=est:602542289F1 /CLONE=IMAGE:4673182 /UG=Hs.203213 ESTs	228716_at
ESTs	Consensus includes gb:AI559300 /FEA=EST /DB_XREF=gi:4509505 /DB_XREF=est:tq43d03.x1 /CLONE=IMAGE:2211557 /UG=Hs.294140 ESTs	229331_at
hypothetical protein	Consensus includes gb:AI830823 /FEA=EST /DB_XREF=gi:5451416 /DB_XREF=est:wj52b06.x1 /CLONE=IMAGE:2406419 /UG=Hs.95549 hypothetical protein	229439_s_at
ESTs	Consensus includes gb:BF431989 /FEA=EST /DB_XREF=gi:11444103 /DB_XREF=est:nab84a05.x1 /CLONE=IMAGE:3274280 /UG=Hs.203213 ESTs	229657_at
ESTs	Consensus includes gb:BF589413 /FEA=EST	229893_at

	/DB_XREF=gi:11681737 /DB_XREF=est:nab26b11.x1 /CLONE=IMAGE:3267020 /UG=Hs.55501 ESTs	
brain-specific protein p25 alpha	Consensus includes gb:BG055052 /FEA=EST /DB_XREF=gi:12512386 /DB_XREF=est:nac94g06.x1 /CLONE=IMAGE:3441995 /UG=Hs.29353 brain-specific protein p25 alpha	230104_s_at
ESTs, Weakly similar to MMHUE4 erythrocyte membrane protein 4.1, parent splice form [H.sapiens]	Consensus includes gb:BF110588 /FEA=EST /DB_XREF=gi:10940278 /DB_XREF=est:7n39e12.x1 /CLONE=IMAGE:3567071 /UG=Hs.150478 ESTs, Weakly similar to KIAA0987 protein H.sapiens	230645_at
ESTs	Consensus includes gb:BF592062 /FEA=EST /DB_XREF=gi:11684386 /DB_XREF=est:7n98h06.x1 /CLONE=IMAGE:3572962 /UG=Hs.233890 ESTs	230760_at
hepatocyte nuclear factor 4, alpha	Consensus includes gb:AI032108 /FEA=EST /DB_XREF=gi:3250320 /DB_XREF=est:ow92d11.x1 /CLONE=IMAGE:1654293 /UG=Hs.54424 hepatocyte nuclear factor 4, alpha	230914_at
ESTs	Consensus includes gb:AW203959 /FEA=EST /DB_XREF=gi:6503431 /DB_XREF=est:UI-H- BI1-aeu-b-12-0-UI.s1 /CLONE=IMAGE:2720590 /UG=Hs.149532 ESTs	230944_at
ESTs	Consensus includes gb:AI139990 /FEA=EST /DB_XREF=gi:3647447 /DB_XREF=est:qa47d03.x1 /CLONE=IMAGE:1689893 /UG=Hs.134586 ESTs	231022_at
ESTs	Consensus includes gb:AI806131 /FEA=EST /DB_XREF=gi:5392697 /DB_XREF=est:wf06c06.x1 /CLONE=IMAGE:2349802 /UG=Hs.99376 ESTs	231148_at
hypothetical protein FLJ23045	Consensus includes gb:AB046810.1 /DEF=Homo sapiens mRNA for KIAA1590 protein, partial cds. /FEA=mRNA /GEN=KIAA1590 /PROD=KIAA1590 protein /DB_XREF=gi:10047254 /UG=Hs.101774 hypothetical protein FLJ23045	232083_at

Homo sapiens PAC clone RP5- 855D21	Consensus includes gb:AC004908 /DEF=Homo sapiens PAC clone RP5-855D21 /FEA=CDS_3 /DB_XREF=gi:4156179 /UG=Hs.249181 Homo sapiens PAC clone RP5-855D21	232641_at
putative microtubule- binding protein	Consensus includes gb:AJ251708.1 /DEF=Homo sapiens partial mRNA for putative microtubule-binding protein. /FEA=mRNA /PROD=putative microtubule-binding protein /DB_XREF=gi:6491740 /UG=Hs.326544 putative microtubule-binding protein	234669_x_at
ESTs	Consensus includes gb:AI741469 /FEA=EST /DB_XREF=gi:5109757 /DB_XREF=est:wg11b01.x1 /CLONE=IMAGE:2364745 /UG=Hs.57787 ESTs	234970_at
ESTs	Consensus includes gb:AI417897 /FEA=EST /DB_XREF=gi:4261401 /DB_XREF=est:tg55b06.x1 /CLONE=IMAGE:2112659 /UG=Hs.235860 ESTs	235444_at
ESTs	Consensus includes gb:AI493909 /FEA=EST /DB_XREF=gi:4394912 /DB_XREF=est:qz94e02.x1 /CLONE=IMAGE:2042234 /UG=Hs.6131 ESTs	235562_at
ESTs	Consensus includes gb:AV741130 /FEA=EST /DB_XREF=gi:10858711 /DB_XREF=est:AV741130 /CLONE=CBCATB06 /UG=Hs.173704 ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens	235651_at
ESTs	Consensus includes gb:AW339510 /FEA=EST /DB_XREF=gi:6836136 /DB_XREF=est:xz91h08.x1 /CLONE=IMAGE:2871615 /UG=Hs.42722 ESTs	235866_at
ESTs	Consensus includes gb:AI076192 /FEA=EST /DB_XREF=gi:3405370 /DB_XREF=est:oz01g07.x1 /CLONE=IMAGE:1674108 /UG=Hs.131933 ESTs	236422_at
ESTs	Consensus includes gb:AL044570 /FEA=EST /DB_XREF=gi:5432785 /DB_XREF=est:DKFZp434L082_s1 /CLONE=DKFZp434L082 /UG=Hs.147975 ESTs	236548_at

ESTs	Consensus includes gb:AI733801 /FEA=EST /DB_XREF=gi:5054914 /DB_XREF=est:qk39c04.x5 /CLONE=IMAGE:1871334 /UG=Hs.146186 ESTs	237923_at
Homo sapiens, clone MGC:16402 IMAGE:394036 0, mRNA, complete cds	Consensus includes gb:T69015 /FEA=EST /DB_XREF=gi:680163 /DB_XREF=est:yc31f04.s1 /CLONE=IMAGE:82303 /UG=Hs.192728 ESTs	238422_at
ESTs	Consensus includes gb:AA502384 /FEA=EST /DB_XREF=gi:2237351 /DB_XREF=est:ne27f11.s1 /CLONE=IMAGE:898605 /UG=Hs.151529 ESTs	238956_at
ESTs	Consensus includes gb:AI739241 /FEA=EST /DB_XREF=gi:5101222 /DB_XREF=est:wi14h02.x1 /CLONE=IMAGE:2390259 /UG=Hs.171480 ESTs	238984_at
ESTs	Consensus includes gb:AA088446 /FEA=EST /DB_XREF=gi:1633958 /DB_XREF=est:zl89f04.s1 /CLONE=IMAGE:511807 /UG=Hs.170298 ESTs	239065_at
ESTs	Consensus includes gb:AI493046 /FEA=EST /DB_XREF=gi:4394049 /DB_XREF=est:qz49b04.x1 /CLONE=IMAGE:2030191 /UG=Hs.146133 ESTs	239148_at
ESTs	Consensus includes gb:AI243098 /FEA=EST /DB_XREF=gi:3838495 /DB_XREF=est:qh26e03.x1 /CLONE=IMAGE:1845820 /UG=Hs.178398 ESTs	239966_at
ESTs, Weakly similar to A49175 Motch B protein - mouse [M.musculus]	Consensus includes gb:AI633523 /FEA=EST /DB_XREF=gi:4684853 /DB_XREF=est:th68b11.x1 /CLONE=IMAGE:2123805 /UG=Hs.44705 ESTs	240106_at
betacellulin	Consensus includes gb:AI620677 /FEA=EST /DB_XREF=gi:4629803 /DB_XREF=est:tu85e09.x1 /CLONE=IMAGE:2257864 /UG=Hs.154191 ESTs	241412_at
ESTs	Consensus includes gb:BF696216 /FEA=EST /DB_XREF=gi:11981624	242626_at

	/DB_XREF=est:602124536F1 /CLONE=IMAGE:4281632 /UG=Hs.188724 ESTs	
ESTs	Consensus includes gb:N57929 /FEA=EST /DB_XREF=gi:1201819 /DB_XREF=est:yv61e06.s1 /CLONE=IMAGE:247234 /UG=Hs.48100 ESTs	242978_x_at
ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINAT ION WARNING ENTRY [H.sapiens]	Consensus includes gb:AI457984 /FEA=EST /DB_XREF=gi:4312002 /DB_XREF=est:tj66a04.x1 /CLONE=IMAGE:2146446 /UG=Hs.165900 ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! H.sapiens	243729_at
ESTs	Consensus includes gb:AA581439 /FEA=EST /DB_XREF=gi:2359211 /DB_XREF=est:nh13c10.s1 /CLONE=IMAGE:952242 /UG=Hs.152328 ESTs	244650_at

The two biomarker probe sets A and B were then combined, a total of 161 different probe sets, and the redundant polynucleotides were removed, representing 125 unique polynucleotides which are provided below in Table 4. The Table 4

5 polynucleotides are biomarkers of the invention.

TABLE 4 - Biomarkers

Unigene Title And SEQ ID NO:	Affymetrix Description	Affymetrix probe set
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial) SEQ ID NOS: 1 (DNA) and 126 (amino acid)	gb:NM_005518.1 /DEF=Homo sapiens 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial) (HMGCS2), mRNA. /FEA=mRNA /GEN=HMGCS2 /PROD=3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2(mitochondrial) /DB_XREF=gi:5031750 /UG=Hs.59889 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial) /FL=gb:NM_005518.1	204607_at
ATPase, Class V, type 10B	Consensus includes gb:AW006935 /FEA=EST /DB_XREF=gi:5855713 /DB_XREF=est:wt08b11.x1	214070_s_at

SEQ ID NO: 2 (DNA)	/CLONE=IMAGE:2506845 /UG=Hs.109358 ATPase, Class V, type 10B	
bone morphogenetic protein 2 SEQ ID NOS: 3 (DNA) and 127 (amino acid)	gb:NM_001200.1 /DEF=Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA. /FEA=mRNA /GEN=BMP2 /PROD=bone morphogenetic protein 2 precursor /DB_XREF=gi:4557368 /UG=Hs.73853 bone morphogenetic protein 2 /FL=gb:NM_001200.1	205290_s_at
brain-specific protein p25 alpha SEQ ID NOS: 4 (DNA) and 128 (amino acid)	gb:NM_007030.1 /DEF=Homo sapiens brain- specific protein p25 alpha (p25), mRNA. /FEA=mRNA /GEN=p25 /PROD=brain- specific protein p25 alpha /DB_XREF=gi:5902017 /UG=Hs.29353 brain-specific protein p25 alpha /FL=gb:AB017016.1 gb:NM_007030.1	206179_s_at
branched chain aminotransferase 1, cytosolic SEQ ID NOS: 5 (DNA) and 129 (amino acid)	Consensus includes gb:NM_005504.1 /DEF=Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA. /FEA=CDS /GEN=BCAT1 /PROD=branched chain aminotransferase 1, cytosolic /DB_XREF=gi:5031606 /UG=Hs.157205 branched chain aminotransferase 1, cytosolic /FL=gb:U21551.1 gb:NM_005504.1	214452_at
BTG family, member 2 SEQ ID NOS: 6 (DNA) and 130 (amino acid)	gb:NM_006763.1 /DEF=Homo sapiens BTG family, member 2 (BTG2), mRNA. /FEA=mRNA /GEN=BTG2 /PROD=BTG family, member 2 /DB_XREF=gi:5802987 /UG=Hs.75462 BTG family, member 2 /FL=gb:U72649.1 gb:NM_006763.1	201236_s_at
Carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) SEQ ID NOS: 7 (DNA) and 131 (amino acid)	gb:BC005008.1 /DEF=Homo sapiens, carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen), clone MGC:10467, mRNA, complete cds. /FEA=mRNA /PROD=carcinoembryonic antigen-related cell adhesionmolecule 6 (non-specific cross reacting antigen) /DB_XREF=gi:13477106 /UG=Hs.73848 carcinoembryonic antigen- related cell adhesion molecule 6 (non-specific cross reacting antigen) /FL=gb:BC005008.1 gb:M18216.1 gb:M29541.1 gb:NM_002483.1	203757_s_at
caspase 10, apoptosis- related cysteine protease SEQ ID NOS: 8	gb:NM_001230.1 /DEF=Homo sapiens caspase 10, apoptosis-related cysteine protease (CASP10), mRNA. /FEA=mRNA /GEN=CASP10 /PROD=caspase 10, apoptosis-related cysteine protease	205467_at

(DNA) and 132 (amino acid)	/DB_XREF=gi:4502568 /UG=Hs.5353 caspase 10, apoptosis-related cysteine protease /FL=gb:U60519.1 gb:Nm_001230.1	
CUG triplet repeat, RNA-binding protein 2 SEQ ID NOS: 9 (DNA) and 133 (amino acid)	gb:Nm_006561.1 /DEF=Homo sapiens CUG triplet repeat, RNA-binding protein 2 (CUGBP2), mRNA. /FEA=mRNA /GEN=CUGBP2 /PROD=CUG triplet repeat, RNA-binding protein 2 /DB_XREF=gi:5729815 /UG=Hs.211610 CUG triplet repeat, RNA-binding protein 2 /FL=gb:U69546.1 gb:AF036956.1 gb:AF090694.1 gb:Nm_006561.1	202158_s_at
cystatin S SEQ ID NOS: 10 (DNA) and 134 (amino acid)	gb:Nm_001899.1 /DEF=Homo sapiens cystatin S (CST4), mRNA. /FEA=mRNA /GEN=CST4 /PROD=cystatin S /DB_XREF=gi:4503108 /UG=Hs.56319 cystatin S /FL=gb:Nm_001899.1	206994_at
cystic fibrosis transmembrane conductance regulator, ATP- binding cassette (sub- family C, member 7) SEQ ID NOS: 11 (DNA) and 135 (amino acid)	gb:Nm_000492.2 /DEF=Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA. /FEA=mRNA /GEN=CFTR /PROD=cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) /DB_XREF=gi:6995995 /UG=Hs.663 cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) /FL=gb:Nm_000492.2	205043_at
cytochrome P450, subfamily IIJ (arachidonic acid epoxygenase) polypeptide 2 SEQ ID NOS: 12 (DNA) and 136 (amino acid)	gb:Nm_000775.1 /DEF=Homo sapiens cytochrome P450, subfamily IIJ (arachidonic acid epoxygenase) polypeptide 2 (CYP2J2), mRNA. /FEA=mRNA /GEN=CYP2J2 /PROD=cytochrome P450, subfamily IIJ (arachidonic acid epoxygenase) polypeptide 2 /DB_XREF=gi:4503226 /UG=Hs.152096 cytochrome P450, subfamily IIJ (arachidonic acid epoxygenase) polypeptide 2 /FL=gb:U37143.1 gb:Nm_000775.1	205073_at
dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2) SEQ ID NOS 13 (DNA) and 137 (amino acid)	gb:M80536.1 /DEF=H.sapiens dipeptidyl peptidase IV (DPP4) mRNA, complete cds. /FEA=mRNA /GEN=DPP4 /PROD=dipeptidyl peptidase IV /DB_XREF=gi:181569 /UG=Hs.44926 dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2) /FL=gb:M80536.1 gb:Nm_001935.1	203716_s_at
DKFZP434C091 protein	Consensus includes gb:AL080170.1 /DEF=Homo sapiens mRNA; cDNA	215047_at

SEQ ID NO: 14 (DNA)	DKFZp434C091 (from clone DKFZp434C091); partial cds. /FEA=mRNA /GEN=DKFZp434C091 /PROD=hypothetical protein /DB_XREF=gi:5262639 /UG=Hs.51692 DKFZP434C091 protein	
dopa decarboxylase (aromatic L-amino acid decarboxylase) SEQ ID NO: 15 (DNA)	Consensus includes gb:AW772056 /FEA=EST /DB_XREF=gi:7704118 /DB_XREF=est:hn64g06.x1 /CLONE=IMAGE:3032698 /UG=Hs.150403 dopa decarboxylase (aromatic L-amino acid decarboxylase)	214347_s_at
EphA1 SEQ ID NOS: 16 (DNA) and 138 (amino acid)	gb:NM_005232.1 /DEF=Homo sapiens EphA1 (EPHA1), mRNA. /FEA=mRNA /GEN=EPHA1 /PROD=EphA1 /DB_XREF=gi:4885208 /UG=Hs.89839 EphA1 /FL=gb:M18391.1 gb:NM_005232.1	205977_s_at
ESTs, Moderately similar to AF078844 1 hqp0376 protein [H.sapiens] SEQ ID NO: 17 (DNA)	Consensus includes gb:R06655 /FEA=EST /DB_XREF=gi:757275 /DB_XREF=est:yf10e02.r1 /CLONE=IMAGE:126458 /UG=Hs.188518 ESTs, Moderately similar to AF078844 1 hqp0376 protein H.sapiens	217546_at
ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens] SEQ ID NO: 18 (DNA)	Consensus includes gb:AW675655 /FEA=EST /DB_XREF=gi:7540890 /DB_XREF=est:ba52e01.x1 /CLONE=IMAGE:2900184 /UG=Hs.314158 ESTs	222354_at
fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome) SEQ ID NOS: 19 (DNA) and 139 (amino acid)	gb:NM_022969.1 /DEF=Homo sapiens fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome) (FGFR2), transcript variant 2, mRNA. /FEA=mRNA /GEN=FGFR2 /PROD=fibroblast growth factor receptor 2, isoform 2precursor /DB_XREF=gi:13186252 /UG=Hs.278581 fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome) /FL=gb:NM_022969.1 gb:M97193.1 gb:M80634.1	203638_s_at
FXD domain-containing ion	gb:BC005238.1 /DEF=Homo sapiens, FXD domain-containing ion transport regulator 3,	202489_s_at

transport regulator 3 SEQ ID NOS: 20 (DNA) and 140 (amino acid)	clone MGC:12265, mRNA, complete cds. /FEA=mRNA /PROD=FXDYD domain- containing ion transport regulator3 /DB_XREF=gi:13528881 /UG=Hs.301350 FXDYD domain-containing ion transport regulator 3 /FL=gb:NM_005971.2 gb:BC005238.1	
G protein-coupled receptor 49 SEQ ID NOS: 21 (DNA) and 141 (amino acid)	gb:AF062006.1 /DEF=Homo sapiens orphan G protein-coupled receptor HG38 mRNA, complete cds. /FEA=mRNA /PROD=orphan G protein-coupled receptor HG38 /DB_XREF=gi:3366801 /UG=Hs.285529 G protein-coupled receptor 49 /FL=gb:AF062006.1 gb:AF061444.1 gb:NM_003667.1	210393_at
hairless (mouse) homolog SEQ ID NOS: 22 (DNA) and 142 (amino acid)	gb:NM_018411.1 /DEF=Homo sapiens hairless protein (putative single zinc finger transcription factor protein, responsible for autosomal recessive universal congenital alopecia, HR gene) (HSA277165), mRNA. /FEA=mRNA /GEN=HSA277165 /PROD=hairless protein /DB_XREF=gi:11036651 /UG=Hs.272367 hairless protein (putative single zinc finger transcription factor protein, responsible for autosomal recessive universal congenital alopecia, HR gene) /FL=gb:NM_018411.1	220163_s_at
hemoglobin, alpha 1 SEQ ID NOS: 23 (DNA) and 143 (amino acid)	gb:BC005931.1 /DEF=Homo sapiens, hemoglobin, alpha 2, clone MGC:14541, mRNA, complete cds. /FEA=mRNA /PROD=hemoglobin, alpha 2 /DB_XREF=gi:13543547 /FL=gb:BC005931.1	211745_x_at
hemoglobin, alpha 2 SEQ ID NO: 24 (DNA)	Consensus includes gb:T50399 /FEA=EST /DB_XREF=gi:652259 /DB_XREF=est:yb30b11.s1 /CLONE=IMAGE:72669 /UG=Hs.251577 hemoglobin, alpha 1	214414_x_at
heparanase SEQ ID NOS: 25 (DNA) and 144 (amino acid)	gb:NM_006665.1 /DEF=Homo sapiens heparanase (HPSE), mRNA. /FEA=mRNA /GEN=HPSE /PROD=heparanase /DB_XREF=gi:5729872 /UG=Hs.44227 heparanase /FL=gb:AF165154.1 gb:AF152376.1 gb:NM_006665.1 gb:AF084467.1 gb:AF155510.1	219403_s_at
Hermansky-Pudlak syndrome	Consensus includes gb:AL022313 /DEF=Human DNA sequence from clone RP5-1119A7 on chromosome 22q12.2-12.3	217354_s_at

SEQ ID NOS: 26 (DNA) and 145 (amino acid)	Contains the TXN2 gene for mitochondrial thioredoxin, a novel gene, the EIF3S7 gene for eukaryotic translation initiation factor 3 subunit 7 (zeta, 6667kD) (EIF3-P66), the gene f... /FEA=CDS_3 /DB_XREF=gi:4200326 /UG=Hs.272270 Human DNA sequence from clone RP5-1119A7 on chromosome 22q12.2-12.3 Contains the TXN2 gene for mitochondrial thioredoxin, a novel gene, the EIF3S7 gene for eukaryotic translation initiation factor 3 subunit 7 (zeta, 6667kD) (EIF3-P66), the gene for a nov	
HERV-H LTR- associating 2 SEQ ID NOS: 27 (DNA) and 146 (amino acid)	gb:NM_007072.1 /DEF=Homo sapiens HERV-H LTR-associating 2 (HHLA2), mRNA. /FEA=mRNA /GEN=HHLA2 /PROD=HERV-H LTR-associating 2 /DB_XREF=gi:5901963 /UG=Hs.252351 HERV-H LTR-associating 2 /FL=gb:AF126162.1 gb:NM_007072.1	220812_s_at
Homo sapiens clone 24707 mRNA sequence SEQ ID NO: 28 (DNA)	Consensus includes gb:AW593996 /FEA=EST /DB_XREF=gi:7281254 /DB_XREF=est:hg41g06.x1 /CLONE=IMAGE:2948218 /UG=Hs.124969 Homo sapiens clone 24707 mRNA sequence	213256_at
Homo sapiens mRNA; cDNA DKFZp564D042 (from clone DKFZp564D042) SEQ ID NO: 29 (DNA)	Consensus includes gb:AL049983.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564D042 (from clone DKFZp564D042). /FEA=mRNA /DB_XREF=gi:4884234 /UG=Hs.240136 Homo sapiens mRNA; cDNA DKFZp564D042 (from clone DKFZp564D042)	217288_at
hypothetical protein FLJ20048 SEQ ID NOS: 30 (DNA) and 147 (amino acid)	gb:NM_017640.1 /DEF=Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA. /FEA=mRNA /GEN=FLJ20048 /PROD=hypothetical protein FLJ20048 /DB_XREF=gi:8923056 /UG=Hs.116470 hypothetical protein FLJ20048 /FL=gb:NM_017640.1	219573_at
hypothetical protein FLJ20075 SEQ ID NOS: 31 (DNA) and 148 (amino acid)	gb:NM_017655.1 /DEF=Homo sapiens hypothetical protein FLJ20075 (FLJ20075), mRNA. /FEA=mRNA /GEN=FLJ20075 /PROD=hypothetical protein FLJ20075 /DB_XREF=gi:8923083 /UG=Hs.205058 hypothetical protein FLJ20075 /FL=gb:NM_017655.1	219970_at

interferon consensus sequence binding protein 1 SEQ ID NO: 32 (DNA)	Consensus includes gb:AI073984 /FEA=EST /DB_XREF=gi:3400628 /DB_XREF=est:oy66c05.x1 /CLONE=IMAGE:1670792 /UG=Hs.14453 interferon consensus sequence binding protein 1 /FL=gb:M91196.1 gb:NM_002163.1	204057_at
KIAA0690 protein SEQ ID NO: 33 (DNA)	Consensus includes gb:AK000238.1 /DEF=Homo sapiens cDNA FLJ20231 fis, clone COLF5511, highly similar to AB014590 Homo sapiens mRNA for KIAA0690 protein. /FEA=mRNA /DB_XREF=gi:7020188 /UG=Hs.60103 KIAA0690 protein	216360_x_at
matrilin 3 SEQ ID NOS: 34 (DNA) and 149 (amino acid)	gb:NM_002381.2 /DEF=Homo sapiens matrilin 3 (MATN3) precursor, mRNA. /FEA=mRNA /GEN=MATN3 /PROD=matrilin 3 precursor /DB_XREF=gi:13518040 /UG=Hs.278461 matrilin 3 /FL=gb:NM_002381.2	206091_at
metastasis-associated 1-like 1 SEQ ID NOS: 35 (DNA) and 150 (amino acid)	gb:NM_004739.1 /DEF=Homo sapiens metastasis-associated 1-like 1 (MTA1L1), mRNA. /FEA=mRNA /GEN=MTA1L1 /PROD=metastasis-associated 1-like 1 /DB_XREF=gi:4758739 /UG=Hs.173043 metastasis-associated 1-like 1 /FL=gb:AB016591.1 gb:NM_004739.1 gb:AF295807.1	203444_s_at
mucin 2, intestinal/tracheal SEQ ID NOS: 36 (DNA) and 151 (amino acid)	gb:NM_002457.1 /DEF=Homo sapiens mucin 2, intestinaltracheal (MUC2), mRNA. /FEA=mRNA /GEN=MUC2 /PROD=mucin 2, intestinaltracheal /DB_XREF=gi:4505284 /UG=Hs.315 mucin 2, intestinaltracheal /FL=gb:NM_002457.1 gb:L21998.1	204673_at
mucin 3B SEQ ID NOS: 37 (DNA) and 152 (amino acid)	Consensus includes gb:AB038783.1 /DEF=Homo sapiens MUC3B mRNA for intestinal mucin, partial cds. /FEA=mRNA /GEN=MUC3B /PROD=intestinal mucin /DB_XREF=gi:9929917 /UG=Hs.129782 mucin 3A, intestinal	214898_x_at
myosin, heavy polypeptide 13, skeletal muscle SEQ ID NOS: 38 (DNA) and 153 (amino acid)	gb:NM_003802.1 /DEF=Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA. /FEA=mRNA /GEN=MYH13 /PROD=myosin, heavy polypeptide 13, skeletal muscle /DB_XREF=gi:11321578 /UG=Hs.278488 myosin, heavy polypeptide 13, skeletal muscle /FL=gb:NM_003802.1 gb:AF111782.2	208208_at

<p>myosin, light polypeptide 5, regulatory</p> <p>SEQ ID NOS: 39 (DNA) and 154 (amino acid)</p>	<p>gb:NM_002477.1 /DEF=Homo sapiens myosin, light polypeptide 5, regulatory (MYL5), mRNA. /FEA=mRNA /GEN=MYL5 /PROD=myosin, light polypeptide 5, regulatory /DB_XREF=gi:4505304 /UG=Hs.170482 myosin, light polypeptide 5, regulatory /FL=gb:L03785.1 gb:NM_002477.1</p>	205145_s_at
<p>nuclear receptor subfamily 3, group C, member 2</p> <p>SEQ ID NOS: 40 (DNA) and 155 (amino acid)</p>	<p>gb:NM_000901.1 /DEF=Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA. /FEA=mRNA /GEN=NR3C2 /PROD=nuclear receptor subfamily 3, group C, member 2 /DB_XREF=gi:4505198 /UG=Hs.1790 nuclear receptor subfamily 3, group C, member 2 /FL=gb:M16801.1 gb:NM_000901.1</p>	205259_at
<p>nuclear receptor subfamily 5, group A, member 2</p> <p>SEQ ID NOS: 41 (DNA) and 156 (amino acid)</p>	<p>Consensus includes gb:AF228413.1 /DEF=Homo sapiens hepatocyte transcription factor mRNA, 3UTR. /FEA=mRNA /DB_XREF=gi:7677372 /UG=Hs.183123 nuclear receptor subfamily 5, group A, member 2 /FL=gb:U93553.1 gb:AB019246.1 gb:AF124247.1</p>	210174_at
<p>pancreas-enriched phospholipase C</p> <p>SEQ ID NOS: 42 (DNA) and 157 (amino acid)</p>	<p>gb:NM_016341.1 /DEF=Homo sapiens pancreas-enriched phospholipase C (LOC51196), mRNA. /FEA=mRNA /GEN=LOC51196 /PROD=pancreas-enriched phospholipase C /DB_XREF=gi:7705940 /UG=Hs.6733 pancreas-enriched phospholipase C /FL=gb:AF190642.2 gb:AF117948.1 gb:NM_016341.1</p>	205112_at
<p>peroxisomal trans 2-enoyl CoA reductase; putative short chain alcohol dehydrogenase</p> <p>SEQ ID NOS: 43 (DNA) and 158 (amino acid)</p>	<p>gb:NM_018441.1 /DEF=Homo sapiens peroxisomal trans 2-enoyl CoA reductase; putative short chain alcohol dehydrogenase (HSA250303), mRNA. /FEA=mRNA /GEN=HSA250303 /PROD=peroxisomal trans 2-enoyl CoA reductase; putative short chain alcohol dehydrogenase /DB_XREF=gi:8923751 /UG=Hs.281680 peroxisomal trans 2-enoyl CoA reductase; putative short chain alcohol dehydrogenase /FL=gb:NM_018441.1</p>	221142_s_at
<p>phosducin</p> <p>SEQ ID NOS: 44 (DNA) and 159 (amino acid)</p>	<p>gb:M33478.1 /DEF=Human 33-kDa phototransducing protein mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:177186 /UG=Hs.550 phosducin /FL=gb:NM_022577.1 gb:M33478.1</p>	211496_s_at

	gb:AF076465.1	
phosphatase and tensin homolog (mutated in multiple advanced cancers 1) SEQ ID NOS: 45 (DNA) and 160 (amino acid)	gb:NM_000314.1 /DEF=Homo sapiens phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN), mRNA. /FEA=mRNA /GEN=PTEN /PROD=phosphatase and tensin homolog (mutated in multiple advanced cancers 1) /DB_XREF=gi:4506248 /UG=Hs.10712 phosphatase and tensin homolog (mutated in multiple advanced cancers 1) /FL=gb:U92436.1 gb:U93051.1 gb:U96180.1 gb:NM_000314.1	204054_at
potassium channel, subfamily K, member 1 (TWIK-1) SEQ ID NOS: 46 (DNA) and 161 (amino acid)	gb:U90065.1 /DEF=Human potassium channel KCNO1 mRNA, complete cds. /FEA=mRNA /PROD=potassium channel KCNO1 /DB_XREF=gi:1916294 /UG=Hs.79351 potassium channel, subfamily K, member 1 (TWIK-1) /FL=gb:U33632.1 gb:U90065.1 gb:U76996.1 gb:NM_002245.1	204678_s_at
prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) SEQ ID NOS: 47 (DNA) and 162 (amino acid)	gb:NM_000963.1 /DEF=Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin GH synthase and cyclooxygenase) (PTGS2), mRNA. /FEA=mRNA /GEN=PTGS2 /PROD=prostaglandin-endoperoxide synthase 2 (prostaglandin GH synthase and cyclooxygenase) /DB_XREF=gi:4506264 /UG=Hs.196384 prostaglandin-endoperoxide synthase 2 (prostaglandin GH synthase and cyclooxygenase) /FL=gb:M90100.1 gb:L15326.1 gb:NM_000963.1	204748_at
protease inhibitor 3, skin-derived (SKALP) SEQ ID NOS: 48 (DNA) and 163 (amino acid)	gb:NM_002638.1 /DEF=Homo sapiens protease inhibitor 3, skin-derived (SKALP) (PI3), mRNA. /FEA=mRNA /GEN=PI3 /PROD=protease inhibitor 3, skin-derived (SKALP) /DB_XREF=gi:4505786 /UG=Hs.112341 protease inhibitor 3, skin-derived (SKALP) /FL=gb:NM_002638.1	203691_at
PTPRF interacting protein, binding protein 2 (liprin beta 2) SEQ ID NO: 49 (DNA)	Consensus includes gb:AI692180 /FEA=EST /DB_XREF=gi:4969520 /DB_XREF=est:wd37f06.x1 /CLONE=IMAGE:2330339 /UG=Hs.12953 PTPRF interacting protein, binding protein 2 (liprin beta 2)	212841_s_at
retinoic acid receptor responder (tazarotene induced) 1	Consensus includes gb:AI669229 /FEA=EST /DB_XREF=gi:4834003 /DB_XREF=est:wc13e06.x1	221872_at

SEQ ID NO: 50 (DNA)	/CLONE=IMAGE:2315074 /UG=Hs.82547 retinoic acid receptor responder (tazarotene induced) 1	
Rho GTPase activating protein 8 SEQ ID NOS: 51 (DNA) and 164 (amino acid)	gb:NM_015366.1 /DEF=Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), mRNA. /FEA=mRNA /GEN=ARHGAP8 /PROD=Rho GTPase activating protein 8 /DB_XREF=gi:7656903 /UG=Hs.102336 Rho GTPase activating protein 8 /FL=gb:NM_015366.1	205980_s_at
ribonuclease, RNase A family, 1 (pancreatic) SEQ ID NOS: 52 (DNA) and 165 (amino acid)	gb:NM_002933.1 /DEF=Homo sapiens ribonuclease, RNase A family, 1 (pancreatic) (RNASE1), mRNA. /FEA=mRNA /GEN=RNASE1 /PROD=ribonuclease, RNase A family, 1 (pancreatic) /DB_XREF=gi:4506546 /UG=Hs.78224 ribonuclease, RNase A family, 1 (pancreatic) /FL=gb:BC005324.1 gb:NM_002933.1 gb:D26129.1	201785_at
serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5 SEQ ID NOS: 53 (DNA) and 166 (amino acid)	gb:NM_002639.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5 (SERPINB5), mRNA. /FEA=mRNA /GEN=SERPINB5 /PROD=serine (or cysteine) proteinase inhibitor, cladeB (ovalbumin), member 5 /DB_XREF=gi:4505788 /UG=Hs.55279 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5 /FL=gb:NM_002639.1 gb:U04313.1	204855_at
spondin 1, (f-spondin) extracellular matrix protein SEQ ID NO: 54 (DNA)	Consensus includes gb:AI885290 /FEA=EST /DB_XREF=gi:5590454 /DB_XREF=est:wl92a04.x1 /CLONE=IMAGE:2432334 /UG=Hs.5378 spondin 1, (f-spondin) extracellular matrix protein	213994_s_at
superoxide dismutase 3, extracellular SEQ ID NOS: 55 (DNA) and 167 (amino acid)	gb:NM_003102.1 /DEF=Homo sapiens superoxide dismutase 3, extracellular (SOD3), mRNA. /FEA=mRNA /GEN=SOD3 /PROD=superoxide dismutase 3, extracellular /DB_XREF=gi:4507150 /UG=Hs.2420 superoxide dismutase 3, extracellular /FL=gb:J02947.1 gb:NM_003102.1	205236_x_at
tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	gb:BC002794.1 /DEF=Homo sapiens, tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator), clone MGC:3753, mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor receptor superfamily, member 14 (herpesvirus	209354_at

SEQ ID NOS: 56 (DNA) and 168 (amino acid)	entry mediator) /DB_XREF=gi:12803894 /UG=Hs.279899 tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator) /FL=gb:BC002794.1 gb:U70321.1 gb:U81232.1 gb:Nm_003820.1 gb:AF153978.1	
tumor necrosis factor receptor superfamily, member 6 SEQ ID NOS: 57 (DNA) and 169 (amino acid)	gb:Nm_000043.1 /DEF=Homo sapiens tumor necrosis factor receptor superfamily, member 6 (TNFRSF6), mRNA. /FEA=mRNA /GEN=TNFRSF6 /PROD=apoptosis (APO-1) antigen 1 /DB_XREF=gi:4507582 /UG=Hs.82359 tumor necrosis factor receptor superfamily, member 6 /FL=gb:M67454.1 gb:Nm_000043.1	204781_s_at
zinc finger protein 137 (clone pHZ-30) SEQ ID NOS: 58 (DNA) and 170 (amino acid)	gb:Nm_003438.1 /DEF=Homo sapiens zinc finger protein 137 (clone pHZ-30) (ZNF137), mRNA. /FEA=mRNA /GEN=ZNF137 /PROD=zinc finger protein 137 (clone pHZ- 30) /DB_XREF=gi:4507988 /UG=Hs.151689 zinc finger protein 137 (clone pHZ-30) /FL=gb:Nm_003438.1 gb:U09414.1	207394_at
hypothetical protein FLJ22233 SEQ ID NO: 59 (DNA)	Consensus includes gb:AI339568 /FEA=EST /DB_XREF=gi:4076495 /DB_XREF=est:qk67e10.x1 /CLONE=IMAGE:1874058 /UG=Hs.286194 hypothetical protein FLJ22233 /FL=gb:Nm_024959.1	222727_s_at
regenerating gene type IV SEQ ID NOS: 60 (DNA) and 171 (amino acid)	gb:AY007243.1 /DEF=Homo sapiens regenerating gene type IV mRNA, complete cds. /FEA=mRNA /PROD=regenerating gene type IV /DB_XREF=gi:12621025 /UG=Hs.105484 Homo sapiens regenerating gene type IV mRNA, complete cds /FL=gb:AY007243.1	223447_at
Homo sapiens cDNA: FLJ21962 fis, clone HEP05564 SEQ ID NO: 61 (DNA)	Consensus includes gb:AK025615.1 /DEF=Homo sapiens cDNA: FLJ21962 fis, clone HEP05564. /FEA=mRNA /DB_XREF=gi:10438186 /UG=Hs.7567 Homo sapiens cDNA: FLJ21962 fis, clone HEP05564	225285_at
ESTs SEQ ID NO: 62 (DNA)	Consensus includes gb:N37023 /FEA=EST /DB_XREF=gi:1158165 /DB_XREF=est:yy40d03.s1 /CLONE=IMAGE:273701 /UG=Hs.235883 ESTs	225407_at
phosphoprotein associated with glycosphingolipid-	Consensus includes gb:AK000680.1 /DEF=Homo sapiens cDNA FLJ20673 fis, clone KAIA4464. /FEA=mRNA	225626_at

enriched microdomains SEQ ID NOS: 63 (DNA) and 172 (amino acid)	/DB_XREF=gi:7020924 /UG=Hs.266175 phosphoprotein associated with GEMs /FL=gb:AF240634.1 gb:NM_018440.1	
prostate cancer associated protein 7 SEQ ID NO: 64 (DNA)	Consensus includes gb:AA633076 /FEA=EST /DB_XREF=gi:2556490 /DB_XREF=est:nq38a06.s1 /CLONE=IMAGE:1146130 /UG=Hs.27495 prostate cancer associated protein 7	226167_at
Homo sapiens, Similar to RIKEN cDNA 1110060O18 gene, clone MGC:17236 IMAGE:3864137, mRNA, complete cds SEQ ID NO: 65 (DNA)	Consensus includes gb:AA524690 /FEA=EST /DB_XREF=gi:2265618 /DB_XREF=est:ng38e07.s1 /CLONE=IMAGE:937092 /UG=Hs.294143 ESTs, Weakly similar to predicted using Genefinder C.elegans	226168_at
hypothetical protein FLJ20209 SEQ ID NO: 66 (DNA)	Consensus includes gb:BF111925 /FEA=EST /DB_XREF=gi:10941704 /DB_XREF=est:7138g05.x1 /CLONE=IMAGE:3523784 /UG=Hs.3685 hypothetical protein FLJ20209	226171_at
Homo sapiens mRNA for KIAA1190 protein, partial cds SEQ ID NOS: 67 (DNA) and 173 (amino acid)	Consensus includes gb:AA532640 /FEA=EST /DB_XREF=gi:2276894 /DB_XREF=est:nj17c04.s1 /CLONE=IMAGE:986598 /UG=Hs.206259 Homo sapiens mRNA for KIAA1190 protein, partial cds	226484_at
KIAA1543 protein SEQ ID NOS: 68 (DNA) and 174 (amino acid)	Consensus includes gb:AB040976.1 /DEF=Homo sapiens mRNA for KIAA1543 protein, partial cds. /FEA=mRNA /GEN=KIAA1543 /PROD=KIAA1543 protein /DB_XREF=gi:7959352 /UG=Hs.17686 KIAA1543 protein	226494_at
hypothetical protein MGC20702 SEQ ID NO: 69 (DNA)	Consensus includes gb:AK002203.1 /DEF=Homo sapiens cDNA FLJ11341 fis, clone PLACE1010786. /FEA=mRNA /DB_XREF=gi:7023932 /UG=Hs.10260 Homo sapiens cDNA FLJ11341 fis, clone PLACE1010786	226992_at
Homo sapiens cDNA FLJ13137 fis, clone NT2RP3003150	Consensus includes gb:AA129774 /FEA=EST /DB_XREF=gi:1690185 /DB_XREF=est:zl16h09.s1	227019_at

SEQ ID NO: 70 (DNA)	/CLONE=IMAGE:502145 /UG=Hs.288905 Homo sapiens cDNA FLJ13137 fis, clone NT2RP3003150	
hypothetical protein FLJ23563	Consensus includes gb:AW138767 /FEA=EST /DB_XREF=gi:6143085 /DB_XREF=est:UI-H-BI1-aep-a-12-0-UI.s1 /CLONE=IMAGE:2719799 /UG=Hs.274256 hypothetical protein FLJ23563	227180_at
SEQ ID NO: 71 (DNA)		
ESTs	Consensus includes gb:AW264333 /FEA=EST /DB_XREF=gi:6641075 /DB_XREF=est:xq98e01.x1 /CLONE=IMAGE:2758680 /UG=Hs.21835 ESTs	227320_at
SEQ ID NO: 72 (DNA)		
ESTs	Consensus includes gb:BF589359 /FEA=EST /DB_XREF=gi:11681683 /DB_XREF=est:nab25d01.x1 /CLONE=IMAGE:3266737 /UG=Hs.13256 ESTs	227354_at
SEQ ID NO: 73 (DNA)		
Homo sapiens, Similar to RIKEN cDNA 1810037C20 gene, clone MGC:21481 IMAGE:3852062, mRNA, complete cds	Consensus includes gb:AW001287 /FEA=EST /DB_XREF=gi:5848203 /DB_XREF=est:wu27e06.x1 /CLONE=IMAGE:2521282 /UG=Hs.61265 ESTs, Weakly similar to G786_HUMAN PROTEIN GS3786 H.sapiens	227676_at
SEQ ID NO: 74 (DNA)		
ESTs, Weakly similar to JX0331 laurate omega-hydroxylase [H.sapiens]	Consensus includes gb:AA557324 /FEA=EST /DB_XREF=gi:2327801 /DB_XREF=est:nl81a02.s1 /CLONE=IMAGE:1057034 /UG=Hs.26040 ESTs, Weakly similar to fatty acid omega- hydroxylase H.sapiens	227702_at
SEQ ID NO: 75 (DNA)		
Homo sapiens cDNA: FLJ22063 fis, clone HEP10326	Consensus includes gb:T86159 /FEA=EST /DB_XREF=gi:714511 /DB_XREF=est:yd84h07.s1 /CLONE=IMAGE:114973 /UG=Hs.10450 Homo sapiens cDNA: FLJ22063 fis, clone HEP10326	227724_at
SEQ ID NO: 76 (DNA)		
GalNAc alpha-2, 6- sialyltransferase I, long form	Consensus includes gb:Y11339.2 /DEF=Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form. /FEA=mRNA /PROD=GalNAc alpha-2,6- sialyltransferase I /DB_XREF=gi:7576275 /UG=Hs.105352 GalNAc alpha-2, 6- sialyltransferase I, long form	227725_at
SEQ ID NOS: 77 (DNA) and 175 (amino acid)		

ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens] SEQ ID NO: 78 (DNA)	Consensus includes gb:AI827789 /FEA=EST /DB_XREF=gi:5448449 /DB_XREF=est:wf33a07.x1 /CLONE=IMAGE:2357364 /UG=Hs.100686 ESTs, Weakly similar to JE0350 Anterior gradient-2 H.sapiens	228241_at
ESTs SEQ ID NO: 79 (DNA)	Consensus includes gb:AI700341 /FEA=EST /DB_XREF=gi:4988241 /DB_XREF=est:wd06e10.x1 /CLONE=IMAGE:2327370 /UG=Hs.110406 ESTs	228653_at
ESTs SEQ ID NO: 80 (DNA)	Consensus includes gb:BG494007 /FEA=EST /DB_XREF=gi:1345521 /DB_XREF=est:602542289F1 /CLONE=IMAGE:4673182 /UG=Hs.203213 ESTs	228716_at
anterior gradient 2 (Xenopus laevis) homolog SEQ ID NO: 81 (DNA)	Consensus includes gb:AI922323 /FEA=EST /DB_XREF=gi:5658287 /DB_XREF=est:wn90h03.x1 /CLONE=IMAGE:2453141 /UG=Hs.293380 ESTs	228969_at
Homo sapiens cDNA: FLJ23331 fis, clone HEP12664 SEQ ID NO: 82 (DNA)	Consensus includes gb:AK026984.1 /DEF=Homo sapiens cDNA: FLJ23331 fis, clone HEP12664. /FEA=mRNA /DB_XREF=gi:10439980 /UG=Hs.50742 Homo sapiens cDNA: FLJ23331 fis, clone HEP12664	229021_at
ESTs SEQ ID NO: 83 (DNA)	Consensus includes gb:AI559300 /FEA=EST /DB_XREF=gi:4509505 /DB_XREF=est:tq43d03.x1 /CLONE=IMAGE:2211557 /UG=Hs.294140 ESTs	229331_at
hypothetical protein SEQ ID NO: 84 (DNA)	Consensus includes gb:AI830823 /FEA=EST /DB_XREF=gi:5451416 /DB_XREF=est:wj52b06.x1 /CLONE=IMAGE:2406419 /UG=Hs.95549 hypothetical protein	229439_s_at
ESTs SEQ ID NO: 85 (DNA)	Consensus includes gb:BF431989 /FEA=EST /DB_XREF=gi:11444103 /DB_XREF=est:nab84a05.x1 /CLONE=IMAGE:3274280 /UG=Hs.203213 ESTs	229657_at
ESTs SEQ ID NO: 86 (DNA)	Consensus includes gb:BF589413 /FEA=EST /DB_XREF=gi:11681737 /DB_XREF=est:nab26b11.x1 /CLONE=IMAGE:3267020 /UG=Hs.55501	229893_at

	ESTs	
brain-specific protein p25 alpha SEQ ID NO: 87 (DNA)	Consensus includes gb:BG055052 /FEA=EST /DB_XREF=gi:12512386 /DB_XREF=est:nac94g06.x1 /CLONE=IMAGE:3441995 /UG=Hs.29353 brain-specific protein p25 alpha	230104_s_at
ESTs, Weakly similar to MMHUE4 erythrocyte membrane protein 4.1, parent splice form [H.sapiens] SEQ ID NO: 88 (DNA)	Consensus includes gb:BF110588 /FEA=EST /DB_XREF=gi:10940278 /DB_XREF=est:7n39e12.x1 /CLONE=IMAGE:3567071 /UG=Hs.150478 ESTs, Weakly similar to KIAA0987 protein H.sapiens	230645_at
ESTs SEQ ID NO: 89 (DNA)	Consensus includes gb:BF592062 /FEA=EST /DB_XREF=gi:11684386 /DB_XREF=est:7n98h06.x1 /CLONE=IMAGE:3572962 /UG=Hs.233890 ESTs	230760_at
hepatocyte nuclear factor 4, alpha SEQ ID NO: 90 (DNA)	Consensus includes gb:AI032108 /FEA=EST /DB_XREF=gi:3250320 /DB_XREF=est:ow92d11.x1 /CLONE=IMAGE:1654293 /UG=Hs.54424 hepatocyte nuclear factor 4, alpha	230914_at
ESTs SEQ ID NO: 91 (DNA)	Consensus includes gb:AW203959 /FEA=EST /DB_XREF=gi:6503431 /DB_XREF=est:UI-H-BI1-aeu-b-12-0-UI.s1 /CLONE=IMAGE:2720590 /UG=Hs.149532 ESTs	230944_at
ESTs SEQ ID NO: 92 (DNA)	Consensus includes gb:AI139990 /FEA=EST /DB_XREF=gi:3647447 /DB_XREF=est:qa47d03.x1 /CLONE=IMAGE:1689893 /UG=Hs.134586 ESTs	231022_at
ESTs SEQ ID NO: 93 (DNA)	Consensus includes gb:AI806131 /FEA=EST /DB_XREF=gi:5392697 /DB_XREF=est:wf06c06.x1 /CLONE=IMAGE:2349802 /UG=Hs.99376 ESTs	231148_at
hypothetical protein FLJ23045 SEQ ID NO: 94 (DNA)	Consensus includes gb:AB046810.1 /DEF=Homo sapiens mRNA for KIAA1590 protein, partial cds. /FEA=mRNA /GEN=KIAA1590 /PROD=KIAA1590 protein /DB_XREF=gi:10047254 /UG=Hs.101774 hypothetical protein FLJ23045	232083_at
Homo sapiens cDNA:	Consensus includes gb:AK026404.1	232321_at

FLJ22751 fis, clone KAIA0483, highly similar to AF016692 Homo sapiens small intestinal mucin (MUC3) mRNA SEQ ID NO: 95 (DNA)	/DEF=Homo sapiens cDNA: FLJ22751 fis, clone KAIA0483, highly similar to AF016692 Homo sapiens small intestinal mucin (MUC3) mRNA. /FEA=mRNA /DB_XREF=gi:10439257 /UG=Hs.271819 Homo sapiens cDNA: FLJ22751 fis, clone KAIA0483, highly similar to AF016692 Homo sapiens small intestinal mucin (MUC3) mRNA	
Homo sapiens PAC clone RP5-855D21 SEQ ID NOS: 96 (DNA), 176 (amino acid), 177 (amino acid), and 178 (amino acid)	Consensus includes gb:AC004908 /DEF=Homo sapiens PAC clone RP5-855D21 /FEA=CDS_3 /DB_XREF=gi:4156179 /UG=Hs.249181 Homo sapiens PAC clone RP5-855D21	232641_at
putative microtubule-binding protein SEQ ID NO: 97 (DNA)	Consensus includes gb:AJ251708.1 /DEF=Homo sapiens partial mRNA for putative microtubule-binding protein. /FEA=mRNA /PROD=putative microtubule-binding protein /DB_XREF=gi:6491740 /UG=Hs.326544 putative microtubule-binding protein	234669_x_at
ESTs SEQ ID NO: 98 (DNA)	Consensus includes gb:AI741469 /FEA=EST /DB_XREF=gi:5109757 /DB_XREF=est:wg11b01.x1 /CLONE=IMAGE:2364745 /UG=Hs.57787 ESTs	234970_at
ESTs SEQ ID NO: 99 (DNA)	Consensus includes gb:AI417897 /FEA=EST /DB_XREF=gi:4261401 /DB_XREF=est:tg55b06.x1 /CLONE=IMAGE:2112659 /UG=Hs.235860 ESTs	235444_at
ESTs SEQ ID NO: 100 (DNA)	Consensus includes gb:AA827649 /FEA=EST /DB_XREF=gi:2900090 /DB_XREF=est:od01a12.s1 /CLONE=IMAGE:1357918 /UG=Hs.105317 ESTs	235515_at
ESTs SEQ ID NO: 101 (DNA)	Consensus includes gb:AI493909 /FEA=EST /DB_XREF=gi:4394912 /DB_XREF=est:qz94e02.x1 /CLONE=IMAGE:2042234 /UG=Hs.6131 ESTs	235562_at
ESTs SEQ ID NO: 102 (DNA)	Consensus includes gb:AV741130 /FEA=EST /DB_XREF=gi:10858711 /DB_XREF=est:AV741130 /CLONE=CBCATB06 /UG=Hs.173704	235651_at

	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens	
ESTs, Weakly similar to I38588 reverse transcriptase homolog [H.sapiens] SEQ ID NO: 103 (DNA)	Consensus includes gb:AI864053 /FEA=EST /DB_XREF=gi:5528160 /DB_XREF=est:wj55h10.x1 /CLONE=IMAGE:2406787 /UG=Hs.39972 ESTs, Weakly similar to I38588 reverse transcriptase homolog H.sapiens	235678_at
ESTs SEQ ID NO: 104 (DNA)	Consensus includes gb:AW339510 /FEA=EST /DB_XREF=gi:6836136 /DB_XREF=est:xz91h08.x1 /CLONE=IMAGE:2871615 /UG=Hs.42722 ESTs	235866_at
ESTs SEQ ID NO: 105 (DNA)	Consensus includes gb:AI076192 /FEA=EST /DB_XREF=gi:3405370 /DB_XREF=est:oz01g07.x1 /CLONE=IMAGE:1674108 /UG=Hs.131933 ESTs	236422_at
ESTs SEQ ID NO: 106 (DNA)	Consensus includes gb:AL044570 /FEA=EST /DB_XREF=gi:5432785 /DB_XREF=est:DKFZp434L082_s1 /CLONE=DKFZp434L082 /UG=Hs.147975 ESTs	236548_at
ESTs SEQ ID NO: 107 (DNA)	Consensus includes gb:AI968097 /FEA=EST /DB_XREF=gi:5764915 /DB_XREF=est:wu13a12.x1 /CLONE=IMAGE:2516830 /UG=Hs.131360 ESTs	237835_at
ESTs SEQ ID NO: 108 (DNA)	Consensus includes gb:AI733801 /FEA=EST /DB_XREF=gi:5054914 /DB_XREF=est:qk39c04.x5 /CLONE=IMAGE:1871334 /UG=Hs.146186 ESTs	237923_at
ESTs SEQ ID NO: 109 (DNA)	Consensus includes gb:BF594323 /FEA=EST /DB_XREF=gi:11686647 /DB_XREF=est:7h79g07.x1 /CLONE=IMAGE:3322236 /UG=Hs.158989 ESTs	238103_at
Homo sapiens, clone MGC:16402 IMAGE:3940360, mRNA, complete cds SEQ ID NO: 110 (DNA)	Consensus includes gb:T69015 /FEA=EST /DB_XREF=gi:680163 /DB_XREF=est:yc31f04.s1 /CLONE=IMAGE:82303 /UG=Hs.192728 ESTs	238422_at

ESTs SEQ ID NO: 111 (DNA)	Consensus includes gb:AA502384 /FEA=EST /DB_XREF=gi:2237351 /DB_XREF=est:ne27f11.s1 /CLONE=IMAGE:898605 /UG=Hs.151529 ESTs	238956_at
ESTs SEQ ID NO: 112 (DNA)	Consensus includes gb:AI739241 /FEA=EST /DB_XREF=gi:5101222 /DB_XREF=est:wi14h02.x1 /CLONE=IMAGE:2390259 /UG=Hs.171480 ESTs	238984_at
ESTs SEQ ID NO: 113 (DNA)	Consensus includes gb:AA088446 /FEA=EST /DB_XREF=gi:1633958 /DB_XREF=est:zl89f04.s1 /CLONE=IMAGE:511807 /UG=Hs.170298 ESTs	239065_at
ESTs SEQ ID NO: 114 (DNA)	Consensus includes gb:AI493046 /FEA=EST /DB_XREF=gi:4394049 /DB_XREF=est:qz49b04.x1 /CLONE=IMAGE:2030191 /UG=Hs.146133 ESTs	239148_at
ESTs SEQ ID NO: 115 (DNA)	Consensus includes gb:AI243098 /FEA=EST /DB_XREF=gi:3838495 /DB_XREF=est:qh26e03.x1 /CLONE=IMAGE:1845820 /UG=Hs.178398 ESTs	239966_at
ESTs, Weakly similar to A49175 Motch B protein - mouse [M.musculus] SEQ ID NO: 116 (DNA)	Consensus includes gb:AI633523 /FEA=EST /DB_XREF=gi:4684853 /DB_XREF=est:th68b11.x1 /CLONE=IMAGE:2123805 /UG=Hs.44705 ESTs	240106_at
ESTs SEQ ID NO: 117 (DNA)	Consensus includes gb:AI300126 /FEA=EST /DB_XREF=gi:3959472 /DB_XREF=est:qn54f02.x1 /CLONE=IMAGE:1902075 /UG=Hs.257858 ESTs	240830_at
ESTs SEQ ID NO: 118 (DNA)	Consensus includes gb:AI917390 /FEA=EST /DB_XREF=gi:5637245 /DB_XREF=est:ts79a05.x1 /CLONE=IMAGE:2237456 /UG=Hs.99415 ESTs	240964_at
betacellulin SEQ ID NO: 119 (DNA)	Consensus includes gb:AI620677 /FEA=EST /DB_XREF=gi:4629803 /DB_XREF=est:tu85e09.x1 /CLONE=IMAGE:2257864 /UG=Hs.154191 ESTs	241412_at
ESTs	Consensus includes gb:H05025 /FEA=EST	241874_at

SEQ ID NO: 120 (DNA)	/DB_XREF=gi:868577 /DB_XREF=est:y174g12.s1 /CLONE=IMAGE:43864 /UG=Hs.323767 ESTs	
ESTs SEQ ID NO: 121 (DNA)	Consensus includes gb:AW024656 /FEA=EST /DB_XREF=gi:5878186 /DB_XREF=est:wu78h05.x1 /CLONE=IMAGE:2526201 /UG=Hs.233382 ESTs, Moderately similar to AF119917 62 PRO2822 H.sapiens	242358_at
ESTs SEQ ID NO: 122 (DNA)	Consensus includes gb:BF696216 /FEA=EST /DB_XREF=gi:11981624 /DB_XREF=est:602124536F1 /CLONE=IMAGE:4281632 /UG=Hs.188724 ESTs	242626_at
ESTs SEQ ID NO: 123 (DNA)	Consensus includes gb:N57929 /FEA=EST /DB_XREF=gi:1201819 /DB_XREF=est:yv61e06.s1 /CLONE=IMAGE:247234 /UG=Hs.48100 ESTs	242978_x_at
ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens] SEQ ID NO: 124 (DNA)	Consensus includes gb:AI457984 /FEA=EST /DB_XREF=gi:4312002 /DB_XREF=est:tj66a04.x1 /CLONE=IMAGE:2146446 /UG=Hs.165900 ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! H.sapiens	243729_at
ESTs SEQ ID NO: 125 (DNA)	Consensus includes gb:AA581439 /FEA=EST /DB_XREF=gi:2359211 /DB_XREF=est:nh13c10.s1 /CLONE=IMAGE:952242 /UG=Hs.152328 ESTs	244650_at

Biological Validation of Biomarker Candidates: Modulation of Expression by Treatment with Ligands for EGFR or by Treatment with Inhibitors for EGFR

To validate the significance of the biomarker candidates to predict the activity
5 of the EGFR pathway and thereby the sensitivity of cancer cell to inhibition of EGFR
by therapy, genes that would be regulated by the EGFR pathway were identified.
Demonstration of that property for the EGFR biomarker candidates described above
would add additional credibility as it would link these genes functionally to the EGFR
pathway. Colon cancer and a lung cancer cell lines were treated with epidermal

growth factor, in the absence of serum or, in the presence of serum with the EGFR modulator BMS-461453 or the EGFR modulator cetuximab (also known as C225, a chimeric monoclonal EGFR antibody). To identify genes induced by epidermal growth factor, serum starved cells were treated with 20ng/ml EGF for 0.5, 6, and 18 hours. Control cells were treated with media alone. The expression profiling was performed, and data was analyzed using GeneChip® Expression Analysis software MAS 5.0 (Affymetrix, Santa Clara, California).

Genes inhibited by EGFR antagonists were identified by treating cells in the presence of 10% serum with 0.5uM of BMS-461453 or 1ug/ml or 5ug/ml of C225 for 6 and 24 hours. Cells exposed to 0.05% DMSO were used as the experimental control. Expression profiling was performed, and data were analyzed using GeneChip® Expression Analysis software MAS 5.0.

The gene expression of the inhibitor or EGFR treated cell lines was compared pair-wise to the untreated controls. Polynucleotides from the biomarker list, in which expression was increased two fold with EGFR exposure or decreased two fold with EGFR inhibitor treatment compared to the untreated controls, were considered to be modulated by EGFR. These biomarkers are provided in Table 4. Examples of the biomarkers include EphA1, B-cell translocation gene 2, prostaglandin-endoperoxide synthase 2 and serine (or cysteine) proteinase inhibitor (clade B), which are highly expressed in sensitive cells and up regulated by treatment with EGFR. On the other hand, spondin 1, talin 2 and nuclear receptor subfamily 3 are genes whose expression levels correlate with sensitivity or resistance of colon cancer cell lines and are consistently down regulated by treatment with EGFR inhibitors BMS-461453 and C225. It appears that these biomarkers are likely to be directly or indirectly involved in the EGFR signaling pathway, based on their expression modulation by EGF or EGFR inhibitor treatment.

Identification of Top Biomarkers

In an attempt to further prioritize biomarkers for use in predicting response of cancer cells to treatment with one or more EGFR modulators, the following filter criteria were used on the Table 4 biomarkers to identify a total of fourteen biomarkers (Table 5) as the top biomarkers:

- (1) results from the highly significant correlation of gene expression with IC₅₀:
A p-value < 0.01 in the student TTEST or a Pearson value < - 0.6 described above;
- (2) results from the modulation of expression by EGFR ligand and/or EGFR inhibitor treatment described above; and
- 5 (3) biomarkers supported by literature revealing a direct relationship between the EGFR pathway and the biomarkers.

TABLE 5 - Top Fourteen Biomarkers

Biomarker Name	Literature Support Citation	Induced by EGF/ Inhibited by EGFR antagonist
mucin 2, intestinal/tracheal (MUC2)	J Biol Chem. 2002 Aug 30;277(35):32258-67	Expression inhibited 2 fold by EGFR antagonist in GEO colon cancer cell line
intestinal mucin 3 (MUC3)	No	Expression inhibited 2 fold by EGFR antagonist in GEO colon cancer cell line
Homo sapiens cystic fibrosis transmembrane conductance regulator ATP-binding cassette (sub-family C, member 7) (CFTR)	No	Expression stimulated 2 fold by EGFR in H292 lung cancer cell line
f-spondin (KIAA0762) protein	No	Expression inhibited 2 fold by EGFR antagonist in LOVO colon cancer cell line
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	J Invest Dermatol. 2000 Jan;114(1):83-7	Expression stimulated 3 fold by EGFR in H292 lung cancer cell line
serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5 (SERPINB5)	Electrophoresis. 2001 Aug;22(14):3001-8.	Expression stimulated 2 fold by EGFR in H292 lung cancer cell line
BTG family, member 2 (BTG2)	No	Expression stimulated 2 fold by EGFR in H292 lung cancer cell line
talins 2 (TLN2)	No	Expression inhibited 2 fold by EGFR antagonist in GEO colon cancer cell line
arachidonic acid	J Biol Chem. 1994 Aug	no

epoxygenase	26;269(34):21786-92.	
prostaglandin G/H synthase and cyclooxygenase	J Biol Chem. 1994 Aug 26;269(34):21786-92.	Expression stimulated 6 fold by EGFR in H292 lung cancer cell line
EphA1 (EPHA1)	No	Expression stimulated 2 fold by EGFR in CACO2 colon cancer cell line
hemoglobin, alpha 1 (HBA1)	No	Expression inhibited 2 fold by EGFR antagonist in GEO colon cancer cell line
bone morphogenetic protein 2	Development 2000 Nov;127(22):4993-5005	no
betacellulin (BTC)*	Biochem Biophys Res Commun. 2002 Jun 28;294(5):1040-6	no

*The gene betacellulin showed counter regulation with EGFR expression as defined for the EGFR-A list but had just a p value of 0.04 in the Student's TTest for correlation with IC₅₀. It was still selected as a top biomarker for the strong literature support, as betacellulin is one of the published ligands of EGFR.

5

Utility of Biomarkers

Polynucleotides that correlate to a specific property of a biological system can be used to make predictions about that biological system and other biological systems. To show the predictive utility of biomarkers that correlate to EGFR modulator sensitivity and resistance, these polynucleotides were tested for their ability to predict the response of twenty two colon cancer cell lines to a small molecule EGFR modulator.

The invention includes single biomarkers including, for example, the fourteen top biomarkers which were tested in a voting scheme. For that purpose, the mean expression value was calculated for all fourteen biomarkers. Colon cancer cell lines which showed an expression level above the mean were then voted to be sensitive, and colon cancer cell lines with expression levels below the mean were voted to be resistant. After this procedure, the voting was compared to the actual sensitivity/resistance status according to the definition based on IC₅₀ (see above) and an error rate was calculated. The error rates of the fourteen top biomarkers are shown in Table 6.

TABLE 6 - Error Rates of Fourteen Top Biomarkers

Biomarker Name	Pearsons value	TTEST P value	Prediction error rate
mucin 2,	-0.531	0.0083	20%

intestinal/tracheal (MUC2)			
intestinal mucin 3 (MUC3)	-0.639	0.0004	11.72%
Homo sapiens cystic fibrosis transmembrane conductance regulator ATP-binding cassette (sub-family C, member 7) (CFTR)	-0.646	9E-05	5.9%
f-spondin (KIAA0762) protein	-0.622	0.0004	12.8%
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	-0.575	0.0029	21.75%
serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5 (SERPINB5)	-0.62	0.0028	21.75%
BTG family, member 2 (BTG2)	-0.544	0.0042	20.5%
talin 2 (TLN2)	-0.874	3E-05	8.8%
EphA1 (EPHA1)	-0.647	0.0021	22%
hemoglobin, alpha 1 (HBA1)	-0.744	8E-05	20%
bone morphogenetic protein 2	-0.555	0.0091	31.8%
betacellulin (BTC)	-0.536	0.047	43.5%

The biomarkers talin, the Cystic fibrosis conductance regulator (CFTR), and mucin 3 were the best single biomarkers with error rates below 12%.

5

EXAMPLES:

EXAMPLE 1 - METHODS

IC₅₀ determination--*in vitro* cytotoxicity assay

A small molecule EGFR inhibitor, erlotinib HCl (BMS-461453), was tested for cytotoxicity *in vitro* against a panel of twenty-two human colon cancer cell lines

available from the American Type Culture Collection. Cytotoxicity was assessed in cells by MTS (3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulphenyl)-2H-tetrazolium, inner salt) assay (T.L. Riss et al., 1992, *Mol. Biol. Cell*, 3 (Suppl.):184a).

5 To carry out the assays, the colon cells were plated at 4,000 cell/well in 96 well microtiter plates and 24 hours later serial diluted drugs were added. The concentration range for the EGFR inhibitor was from 5 $\mu\text{g/ml}$ to 0.0016 $\mu\text{g/ml}$ (roughly 10 μM to 0.0032 μM). The cells were incubated at 37 °C for 72 hours at which time the tetrazolium dye MTS (333 $\mu\text{g/ml}$ final concentration) in combination
10 with the electron coupling agent phenazine methosulfate (25 μM final concentration) was added. A dehydrogenase enzyme in live cells reduces the MTS to a form that absorbs light at 492 nm that can be quantified spectrophotometrically. The greater the absorbency, the greater the number of live cells. The results were expressed as an IC_{50} , which is the drug concentration required to inhibit cell proliferation (i.e.,
15 absorbance at 450 nm) to 50% of that of untreated control cells. The mean IC_{50} and standard deviation (SD) from multiple tests for each cell line were calculated.

Resistant/sensitive classification

 The cell lines with IC_{50} below 6 μM were defined as sensitive to the EGFR
20 inhibitor, whereas those with IC_{50} above 6 μM were considered to be resistant. The resistant/sensitive classification are shown above in Table 1, with five cell lines classified as sensitive and seventeen cell lines classified as resistant.

Gene expression profiling

25 The colon cells were grown using standard cell culture conditions: RPMI 1640 supplemented to contain 10% fetal bovine serum, 100 IU/ml penicillin, 100 mg/ml streptomycin, 2 mM L-glutamine and 10 mM Hepes (all from GibcoBRL, Rockville, Maryland). RNA was isolated from 50-70% confluent cells or drug-treated cells using the RNeasy™ kits commercially available from Qiagen (Valencia,
30 California). Quality of the RNA was checked by measuring the 28s:18s ribosomal RNA ratio using Agilent 2100 bioanalyzer (Agilent, Technologies, Rockville, Maryland). Concentration of total RNA was determined spectrophotometrically. 10

µg of total RNA from each cell line was used to prepare biotinylated probe according to the Affymetrix Genechip® Expression Analysis Technical Manual, 2001. Targets were hybridized to Affymetrix high density oligonucleotide array human HG-U133 set chips (Affymetrix, Santa Clara, California). Arrays were then washed, and stained
5 using the GeneChip Fluidics station according to the manufacture's instructions. The HG-U133 set consisting of two GeneChip® arrays contains nearly 45,000 probe sets representing more than 39,000 transcripts derived from approximately 33,000 well-substantiated human genes.

10 Preprocessing of microarray data for selecting biomarkers

Scanned image files were visually inspected for artifacts and analyzed with GeneChip® Expression Analysis software MAS 5.0 (Affymetrix, Santa Clara, California). The “Detection Call” (see Affymetrix manual) was used to determine whether a transcript was detected within one sample, as well as the “Signal” (see
15 Affymetrix Genechip® Expression Analysis Technical Manual, 2001) which measured the relative abundance of a transcript. The trimmed mean intensity for each chip was scaled to 1,500 (see Affymetrix manual) in order to account for any minor differences in global chip intensity, so that the overall expression level for each cell line is comparable. Affymetrix control sequences were removed prior to analysis.

20

Induction Studies of colon and breast cell lines with EGFR inhibitors or EGFR ligand and selection of genes modulated by the inductions

The five colon cell lines and one lung cell line indicated with asterisks in Table 1 were used in the drug induction study. Three of the colon cell lines express
25 EGFR and are sensitive to the EGFR inhibitor BMS-461453. The SW480 cell line, while expressing EGFR, is insensitive to the EGFR inhibitor, and the COLO320_DM does not express EGFR and is EGFR inhibitor resistant. The lung cancer cell line H292 expresses EGFR, but its sensitivity status is unknown. Cells were seeded in a 10 cm² culture plate with the medium described above and cultured for 24 hours.

30 For the EGF induction studies, the colon cell line CACO2 and the lung cancer H292 cell line were washed 2X PBS, and the media was changed to RPMI without serum. The next day the cells were treated with 20 ng/ml EGF, and eventually lysed

for RNA isolation 0.5, 6 and 18 hours post treatment. Gene expression was profiled as described below.

EGFR inhibition studies were conducted on the colon cell lines GEO, CCD33-CO, SW480 and COLO320DM. The expression profiling was performed as
5 described above and data was analyzed using GeneChip® Expression Analysis software MAS 5.0. The expression data of EGFR inhibitor treated cell lines were compared pair-wise to that of untreated same cell line. A change was considered significant if a two fold difference in expression was demonstrated between the treated and the untreated control. Analysis was done for all four cell lines to compare
10 the gene expression with or without EGFR inhibitor treatment.

EXAMPLE 2 - RT-PCR EXPRESSION PROFILING

RNA quantification was performed using the SYBR Green real-time PCR. The SYBR Green real-time PCR assay is one of the most precise methods for
15 assaying the concentration of nucleic acid templates.

RNA can be prepared using standard methods, preferably, employing the RNeasy Kit commercially available from Qiagen (Valencia, California). cDNA template for real-time PCR can be generated using the Superscript™ First Strand Synthesis system for RT-PCR. SYBR Green real-time PCR reactions are prepared as
20 follows: the reaction mix contains 20 ng first strand cDNA; 50 nM Forward Primer; 50 nM Reverse Primer; 0.75X SYBR Green I (Sigma); 1X SYBR Green PCR Buffer (50mM Tris-HCl pH 8.3, 75 mM KCl); 10% DMSO; 3 mM MgCl₂; 300 μM each dATP, dGTP, dTTP, dCTP; 1 U Platinum® Taq DNA Polymerase High Fidelity (Cat# 11304-029; Life Technologies; Rockville, Maryland). Real-time PCR is
25 performed using an Applied Biosystems 5700 Sequence Detection System. Conditions are 95 °C for 10 minutes (denaturation and activation of Platinum® Taq DNA Polymerase), 40 cycles of PCR (95 °C for 15 seconds, 60 °C for 1 minute). PCR products are analyzed for uniform melting using an analysis algorithm built into the 5700 Sequence Detection System.

30 cDNA quantification used in the normalization of template quantity is performed using SYBR Green real-time PCR. Expression of EGFR is normalized to GAPDH expression as described below.

The sequences for the GAPDH oligonucleotides used in the SYBR Green real-time PCR reactions are:

GAPDH-F: 5'-AGCCGAGCCACATCGCT-3' (SEQ ID NO: 191)

GAPDH-R: 5'-GTGACCAGGCGCCCAATAC-3' (SEQ ID NO: 192)

5 The sequences for the EGFR oligonucleotides used in the SYBR Green real-time PCR reactions are:

EGFR-F: 5'-GCGTCTCTTGCCGGAATGT-3' (SEQ ID NO: 193)

EGFR-R: 5'-AGCCGAGGCAGGGAATGCGTG-3' (SEQ ID NO: 194)

10 The Sequence Detection System generates a Ct (threshold cycle) value that is used to calculate a concentration for each input cDNA template. cDNA levels for each gene of interest are normalized to GAPDH cDNA levels to compensate for variations in total cDNA quantity in the input sample. This is done by generating GAPDH Ct values for each cell line. Ct values for the gene of interest and GAPDH are inserted into a modified version of the $\delta\delta Ct$ equation (Applied Biosystems
15 Prism® 5700 Sequence Detection System User Manual) which is used to calculate a GAPDH normalized relative cDNA level for each specific cDNA. The $\delta\delta Ct$ equation is: relative quantity of nucleic acid template $= 2^{\delta\delta Ct} = 2^{(\delta Ct_a - \delta Ct_b)}$, where $\delta Ct_a = Ct$ target – Ct GAPDH, and $\delta Ct_b = Ct$ reference – Ct GAPDH.

20 EXAMPLE 3 - PRODUCTION OF ANTIBODIES AGAINST THE BIOMARKERS

Antibodies against the biomarkers can be prepared by a variety of methods. For example, cells expressing an biomarker polypeptide can be administered to an animal to induce the production of sera containing polyclonal antibodies directed to the expressed polypeptides. In one aspect, the biomarker protein is prepared and
25 isolated or otherwise purified to render it substantially free of natural contaminants, using techniques commonly practiced in the art. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity for the expressed and isolated polypeptide.

In one aspect, the antibodies of the invention are monoclonal antibodies (or
30 protein binding fragments thereof). Cells expressing the biomarker polypeptide can be cultured in any suitable tissue culture medium, however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented to contain 10% fetal bovine

serum (inactivated at about 56 °C), and supplemented to contain about 10 g/l nonessential amino acids, about 1,00 U/ml penicillin, and about 100 µg/ml streptomycin.

5 The splenocytes of immunized (and boosted) mice can be extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line can be employed in accordance with the invention, however, it is preferable to employ the parent myeloma cell line (SP2/0), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (1981, *Gastroenterology*, 80:225-232).
10 The hybridoma cells obtained through such a selection are then assayed to identify those cell clones that secrete antibodies capable of binding to the polypeptide immunogen, or a portion thereof.

Alternatively, additional antibodies capable of binding to the biomarker polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies.
15 Such a method makes use of the fact that antibodies are themselves antigens and, therefore, it is possible to obtain an antibody that binds to a second antibody. In accordance with this method, protein specific antibodies can be used to immunize an animal, preferably a mouse. The splenocytes of such an immunized animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify
20 clones that produce an antibody whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce the formation of further protein-specific antibodies.

25 EXAMPLE 4 - IMMUNOFLUORESCENCE ASSAYS

The following immunofluorescence protocol may be used, for example, to verify EGFR biomarker protein expression on cells or, for example, to check for the presence of one or more antibodies that bind EGFR biomarkers expressed on the surface of cells. Briefly, Lab-Tek II chamber slides are coated overnight at 4 °C with
30 10 micrograms/milliliter (µg/ml) of bovine collagen Type II in DPBS containing calcium and magnesium (DPBS++). The slides are then washed twice with cold DPBS++ and seeded with 8000 CHO-CCR5 or CHO pC4 transfected cells in a total

volume of 125 µl and incubated at 37 °C in the presence of 95% oxygen / 5% carbon dioxide.

The culture medium is gently removed by aspiration and the adherent cells are washed twice with DPBS++ at ambient temperature. The slides are blocked with
5 DPBS++ containing 0.2% BSA (blocker) at 0-4 °C for one hour. The blocking solution is gently removed by aspiration, and 125 µl of antibody containing solution (an antibody containing solution may be, for example, a hybridoma culture supernatant which is usually used undiluted, or serum/plasma which is usually diluted, e.g., a dilution of about 1/100 dilution). The slides are incubated for 1 hour at
10 0-4 °C. Antibody solutions are then gently removed by aspiration and the cells are washed five times with 400 µl of ice cold blocking solution. Next, 125 µl of 1 µg/ml rhodamine labeled secondary antibody (e.g., anti-human IgG) in blocker solution is added to the cells. Again, cells are incubated for 1 hour at 0-4 °C.

The secondary antibody solution is then gently removed by aspiration and the
15 cells are washed three times with 400 µl of ice cold blocking solution, and five times with cold DPBS++. The cells are then fixed with 125 µl of 3.7% formaldehyde in DPBS++ for 15 minutes at ambient temperature. Thereafter, the cells are washed five times with 400 µl of DPBS++ at ambient temperature. Finally, the cells are mounted in 50% aqueous glycerol and viewed in a fluorescence microscope using rhodamine
20 filters.

CLAIMS:

What is claimed is:

1. A method for identifying a mammal that will respond therapeutically to a method of treating cancer comprising administering an EGFR modulator, wherein the method comprises:
 - (a) measuring in the mammal the level of at least one biomarker selected from the biomarkers of Table 4;
 - (b) exposing the mammal to the EGFR modulator;
 - (c) following the exposing of step (b), measuring in the mammal the level of the at least one biomarker,wherein a difference in the level of the at least one biomarker measured in step (c) compared to the level of the at least one biomarker measured in step (a) indicates that the mammal will respond therapeutically to said method of treating cancer.
2. The method of claim 1 wherein the at least one biomarker is selected from the biomarkers of Table 5.
3. The method of claim 1 wherein the method is an in vitro method, and wherein the at least one biomarker is measured in at least one mammalian biological sample from the mammal.
4. A method for identifying a mammal that will respond therapeutically to a method of treating cancer comprising administering an EGFR modulator, wherein the method comprises:
 - (a) exposing the mammal to the EGFR modulator;
 - (b) following the exposing of step (a), measuring in the mammal the level of the at least one biomarker selected from the biomarkers of Table 4,wherein a difference in the level of the at least one biomarker measured in step (b), compared to the level of the biomarker in a mammal that has not been exposed to said EGFR modulator, indicates that the mammal will respond therapeutically to said method of treating cancer.

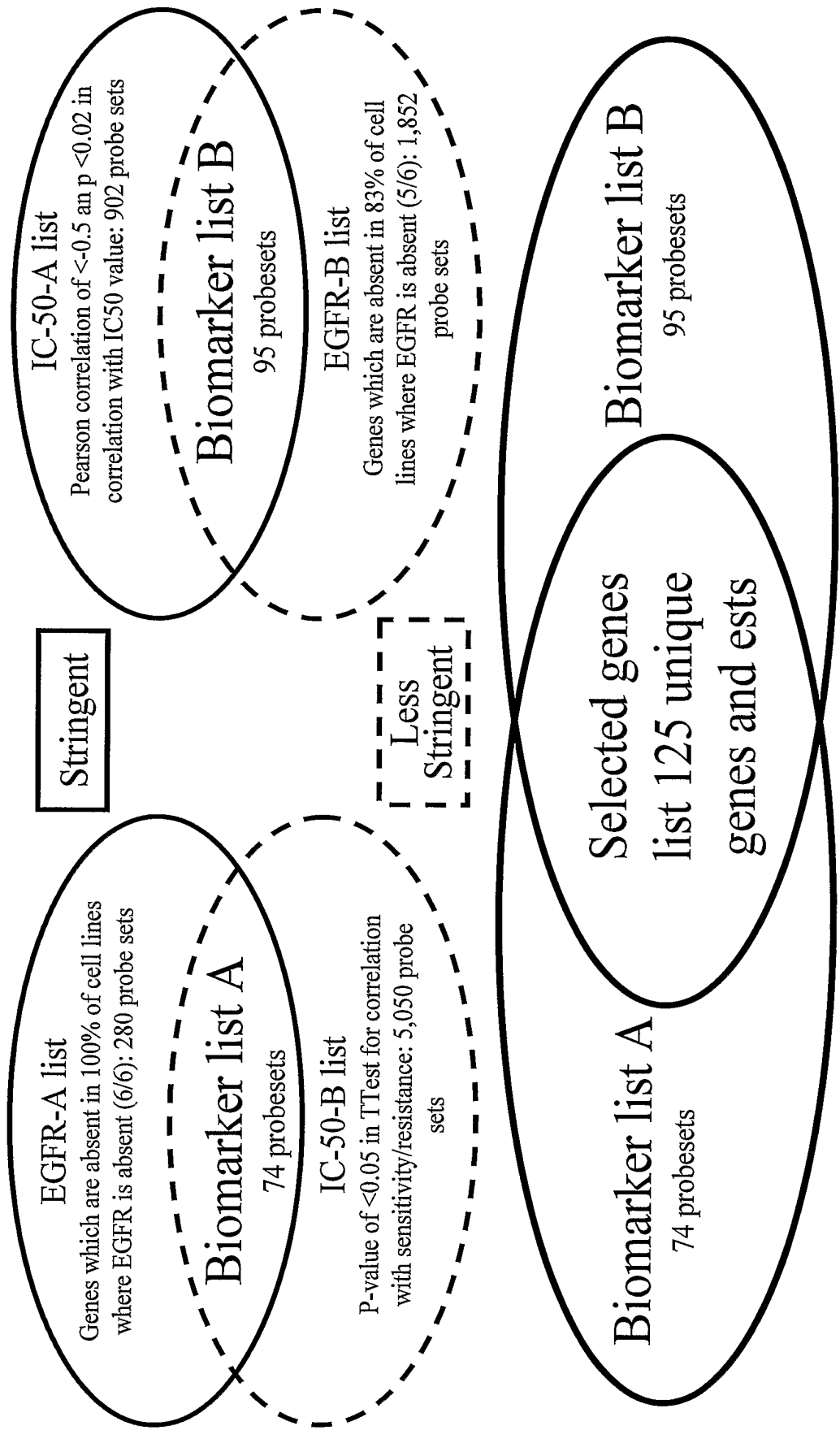


FIG. 1

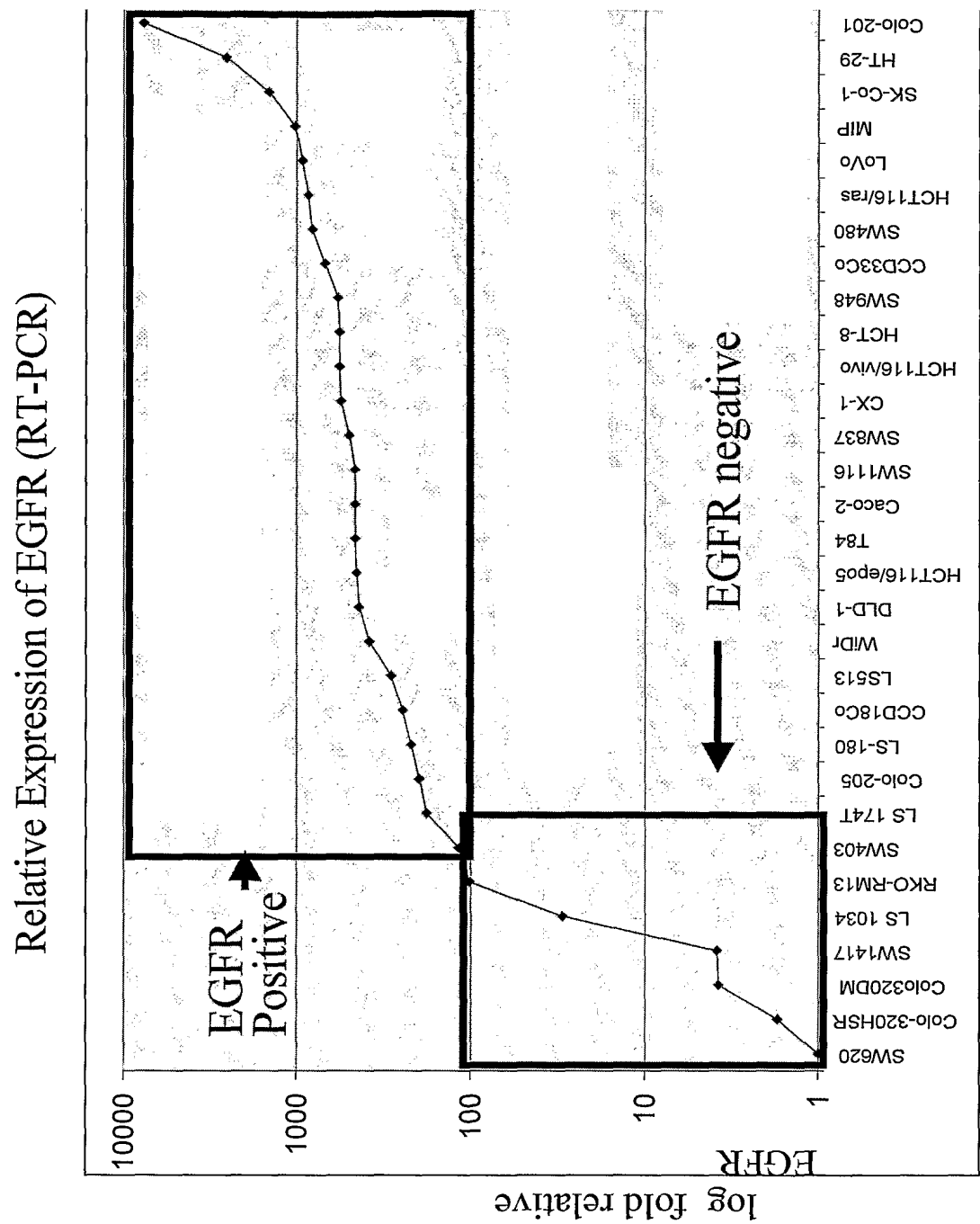


FIG. 2A

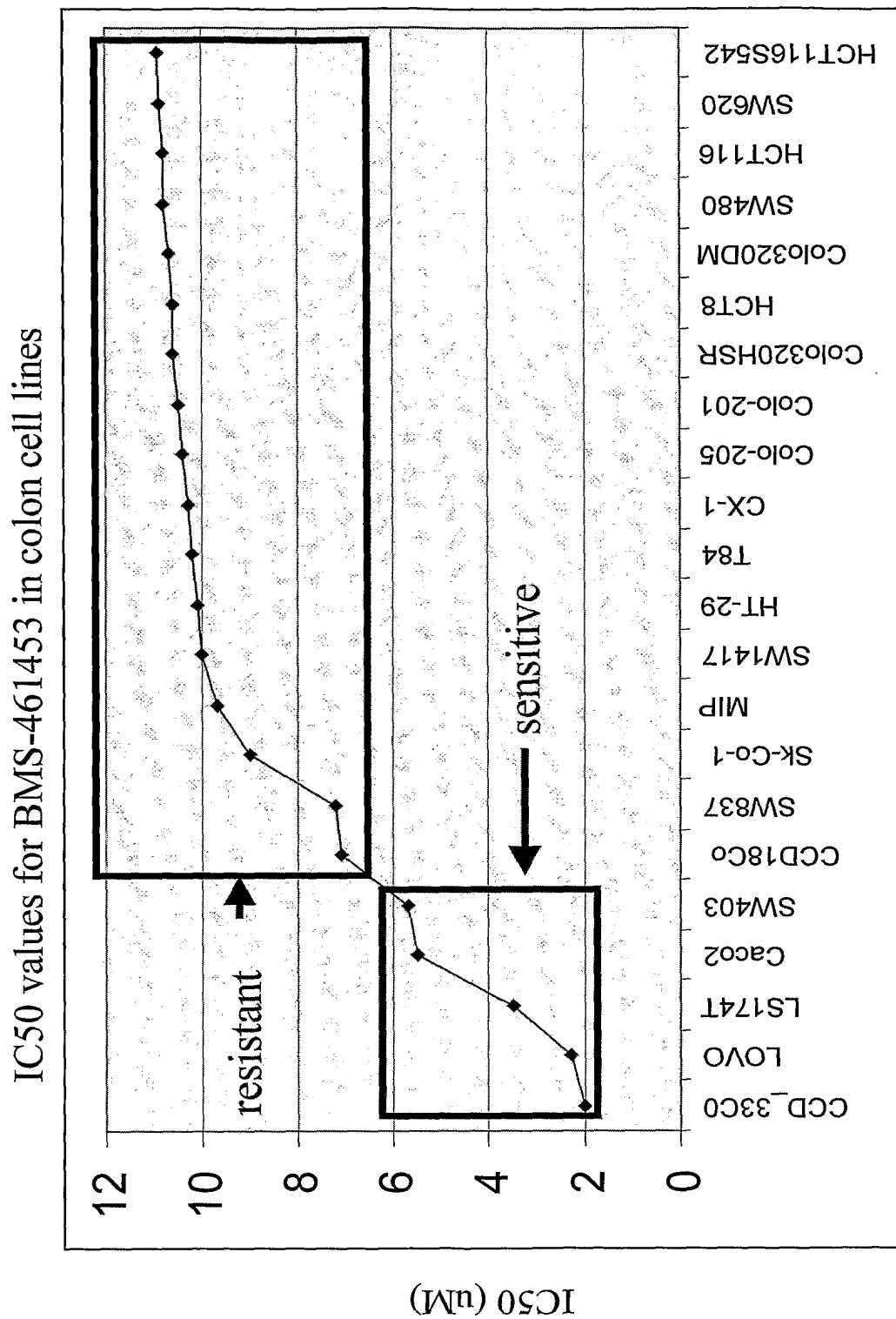


FIG. 2B

SEQUENCE LISTING

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<210> 48
 <211> 631
 <212> DNA
 <213> Human

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<400> 48
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tgagggccag cagcttcttg atcgtggttg tgttcctcat cgctgggacg ctggttctag      180

aggcagctgt cacgggagtt cctgttaaag gtcaagacac tgtcaaaggc cgtgttccat      240

tcaatggaca agatcccggt aaaggacaag tttcagttaa aggtcaagat aaagtcaaag      300

cgcaagagcc agtcaaaggc ccagttotcca ctaagcctgg ctctgcccc attatcttga      360

tccggtgcgc catgttgaat cccoctaacc gctgcttgaa agatactgac tgcccaggaa      420

tcaagaagtg ctgtgaaggc tcttgcgga tggcctgttt cgttccccag tgaagggagc      480

cggtccttgc tgcacctgtg ccgtccccag agctacaggc cccatctggt cctaagtccc      540

tgctgccctt ccccttccca cactgtccat tcttcctccc attcaggatg cccacggctg      600

gagctgcctc tctcatccac tttccaataa a                                     631

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<210> 49
<211> 701
<212> DNA
<213> Human

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<220>
<221> misc_feature
<222> (464)..(464)
<223> n is a, c, g, or t

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<400> 49
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cagccaagac tgtggtccac gggcctaagg cacttgagct tttccctcaa ctgaagtgtg      180

gggggtgcct gagagctgag cctcgtggga gtgtccatgg tctctggacc tgcacgaag      240

ttcatgtgtt tccactgggt ctgaagatga acatcaagaa ttactagaca tgtaaaagtg      300

tctttaagtg tctttcctcc tgagtccacc tttggcaatg gtccccaaag cctggcccct      360

tagagatgca gctccagatc ctggccaccc tcagggttca aagagactgg cccaggggta      420

cacaattgct ggaatatctt ctgcgagtca tgcacacgtg cggnggtgag gtgcagttat      480

atggtgacac acacagtgtt actgtgagct ctcagggtgc acagagggca ggtgacaagg      540

gcatcagcta atctgtccca cctgggtccag cccatccagt tcaggggcat caagggggct      600

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<210> 50
 <211> 602
 <212> DNA
 <213> Human

<400> 50
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 tttcatcgaa agtatattat ctttgtttaa catgctagat agaagcaatt tagcaacata 180
 aaatatatta gctatagtat gttcaaaaga atgagaaata taaattcaga gatgagacca 240
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 gtctatacct tagctgtttt actagaatga tttatgctag tatagtcact tgtttagaag 540
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 cc 602

<210> 51
 <211> 1653
 <212> DNA
 <213> Human

<400> 51
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<210> 52
 <211> 846
 <212> DNA
 <213> Human

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<400> 52
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 tccctgcgtg attttggggg tgaagagtgg gttgtgaggt gggcccatg ttaaccctc 780
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 aaaaaa 846

<210> 53
 <211> 2566
 <212> DNA
 <213> Human

<400> 53
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<210> 54
<211> 555
<212> DNA
<213> Human

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<220>
<221> misc_feature
<222> (9)..(10)
<223> n is a, c, g, or t
<400> 54

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ggaaatctct ctctgaactt cttgctgttg gacctaaaat gtggatgtaa attggatcac    180
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<210> 55
 <211> 1984
 <212> DNA
 <213> Human

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<400> 55
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 ttca 1984

<210> 56
 <211> 1621
 <212> DNA
 <213> Human

<400> 56
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 <213> Human

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<213> Human

<400> 59

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<211> 1130

<212> DNA

<213> Human

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<211> 3323
<212> DNA
<213> Human

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cagctgtgat ttcttttgta gcattctggc tctccacttc tattcatata attgagtatg 540
tgttttatta catgttagct tataggcaag ttaaacad 578

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<210> 72
 <211> 475
 <212> DNA
 <213> Human

<220>
 <221> misc_feature
 <222> (285)..(285)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (361)..(361)

<223> n is a, c, g, or t

<400> 72

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gggtttgcac agtttatttaa gataatcaat caattttctta agttattcct ttgttaacca      60
gacagcatct ctggagagaa aatgcactct ctgtgtagat acataaaaaat acatcagtca      120
ttttgccct cctggatgtg aacggaatct cccctcctca cctccacaga gggagctcaa      180
gccccaggga acottccccct ccccttttat gcattaccag gggagtggca ggggcagccc      240
ccaactgtgg agtgcattca ggtctgaggg gggaggaagg ctcanagggg catctcccca      300
gcacctgcc acagtgtctg cttctggggg gtttgttcag cggcctgctg ggctgccccca      360
ngctgggggc tccccagct ccccgatcat cctggcttgt tccacggagc cctgagccaa      420
gtctttgtct ggctcatgtt cctctcaca catcccacag gcagggggtga gcctg      475

```

<210> 73

<211> 512

<212> DNA

<213> Human

<400> 73

```

catgtaaaac tgacttttat tacaattaaa aaagaacaaa gacaatttga taagtgcctt      60
taattacaac atacctgcta tttacatgta atcatacttt tatatatagc ttgaataagt      120
tttattacat gtaaactata agatattaca agttaaactc cagtcttttc tggatattca      180
attgaaatac tactggcaga aacatacaga aaacaaatac ccatttcagt tcctcaggta      240
ccattactgg ttgaatgatc aagatctggc cacagaagag aagtggaaat atgcatcaaa      300
acaaaactta ttcttaacat gactaacagt attgttatTT aaaccctaaa cataattaat      360
aattggatca ttaaaaacac atcttcaatt tatatagcac ctttcttccg aagagttgaa      420
agcattcgtg cttatctcta ttatttcggt tgtcccata acatctctat gaggtaggca      480
atggttagta tcattatccc cattttgtat at      512

```

<210> 74

<211> 668

<212> DNA

<213> Human

<400> 74

```

tttcaaaacc agcaaaaatt aaatttaatt gggctcaagt ctgggcagtt tgtccttctt      60
caggaccago cgtcagcagt cctgacgaa agcaccocat tctctccaca gacagctggt      120

```

```

tccaaaagga ccctctgagg ctggtcttcc gggtaggatg tgctgtggga gggttctgtt 180
tccgaggagg agaggcgcga cacagcgtgc aaggacctgc agcaccttcc acgcagcacc 240
ccctgctcct cctcctcagc ccctgccggg ctctgactcc taaagtaagg caggagcttc 300
ttcaggcccc tggctgagga agagccacag ccaccctaaa atggcttcgg gggcatgcag 360
ccctccatct ccagcagctc tggccatccc tcgtatttgt tgggtgtctgg gctgttcttt 420
aagaactgct caaaggggct gttacccttg aggtcttttg ctctatgaa gaccagctg 480
tcccgaagc ccagttgttt tgcgtaggaa ctccccaagt cagagaagag tttcctgctt 540
tcctcgatca ttttggtcgc tggatcgctg taggaggcca ccaacaccag tgcacccgc 600
ggaaatatct tatggaattt cactaggtgc ataacttctc ctaagtgcac gtcaaagcc 660
tgctggcg 668

```

```

<210> 75
<211> 568
<212> DNA
<213> Human

```

```

<400> 75
aaggaataag gtgaattttt attaagtga aaaaatcaat aacaatatag gaatgatcac 60
atctatacaa atacattgct acatttctac atataaaatg tataggaaaa agtctgaaag 120
aatgcacacc aaattattct gtttttagga aaagcagtag gattggtcag ggcattggaat 180
gtcggctaag tgaagtgaga tttaaaattt ttattctaca tgattttcta gtgttgggaa 240
tttttgacag tgagcataca tgcacttatt acttgcataa ttctgaaaac tattttaaaa 300
acaacagaga atatatgaaa gtctattggg gtatacagca ttaatagtag tgaaagttaa 360
acagaaaaga tctgaaaatc tcccaaagtt atatagaaac agatctagct gacacactgt 420
gtacctagaa atgatttttg atctcttcac agagaccctt atcccaccaa cctccaatcc 480
tcccaccata cattgatccc tttctatctg cttggatcat tagctgtaaa ttttaacttcg 540
aaaaacaag tacgtttaat cattgtac 568

```

```

<210> 76
<211> 491
<212> DNA
<213> Human

```

```

<220>
<221> misc_feature
<222> (371)..(371)
<223> n is a, c, g, or t

```

<220>

<221> misc_feature

<222> (394)..(394)

<223> n is a, c, g, or t

<400> 76

ttagattgaa gaaaacataa cgtttaattc tcagaaacaa atgcaagcct cgggtccaagt	60
cttccttccc aaacctttgt catttaggga ttgagaagct gagttgggtg aaaggttgaa	120
tagaaaacaa aaaggaaagc tagaaacacg ctgagctcat ggagatgcag cttcttctgt	180
agctcctaaa ggcccagctg aggtatcatc taatgagaat tctctctatg ccaggcactg	240
cgctaagatt ttcacatcat taaccaatgt gagttttagg caaccccgaa gcaggcagtc	300
tgttcatccc aattgcagct gaggaaacag gggtaggtg aggccaagca gctgggcca	360
agggtcccct ncctgggtaa gtgggcacag ctgncagccc tgccagggtg gggctctgct	420
aaccaagccg gcgttttctt gtcaccatgc cgtattcgcc ttcccgctact atcaaatgt	480
acttatccaa t	491

<210> 77

<211> 2437

<212> DNA

<213> Human

<400> 77

tcggatccac tagtaacggc cgccagtgtg ctggaattcg cggccggtcg acccaccacc	60
atgaggctct gcctgtggag atgcaggcac ctgagccaag gcgtccagtg gtccttgett	120
ctggctgtcc tggctttctt tctcttcgcc ttgccctctt ttattaagga gcctcaaaca	180
aagccttcca ggcatcaacg cacagagaac attaaagaaa ggtctctaca gtccctggca	240
aagcctaagt ccaggcacc cacaagggca aggaggacaa ccatctatgc agagccagtg	300
ccagagaaca atgccctcaa cacacaaacc cagcccaagg ccacacccac cggagacaga	360
ggaaaggagg ccaaccaggc accgccggag gagcaggaca aggtgccccca cacagcacag	420
agggcagcat ggaagagccc agaaaaagag aaaaccatgg tgaacacact gtcaccaga	480
gggcaagatg cagggatggc ctctggcagg acagaggcac aatcatggaa gagccaggac	540
acaaagacga cccaaggaaa tgggggccag accaggaagc tgacggcctc caggacggtg	600
tcagagaagc accagggcaa agcggcaacc acagccaaga cgctcattcc caaaagtcag	660
cacagaatgc tggctccac aggagcagtg tcaacaagga cgagacagaa aggagtgacc	720
acagcagtca tcccacctaa ggagaagaaa cctcaggcca cccaccccc tgcccctttc	780
cagagcccca cgacgcagag aaaccaaaga ctgaaggccg ccaacttcaa atctgagcct	840

cggtgggatt ttgaggaaaa atacagcttc gaaataggag gccttcagac gacttgccct	900
gactctgtga agatcaaagc ctccaagtcg ctgtggctcc agaaactott tctgccaac	960
ctcactctct tootggactc cagacacttc aaccagagtg agtgggaccg cctggaacac	1020
tttgcaccac cctttggctt catggagctc aactactcct tgggtgcagaa ggtcgtgaca	1080
cgcttccttc cagtgoccca gcagcagctg ctcttgcca gcctccccgc tgggagcctc	1140
cggtgcatca cctgtgccgt ggtgggcaac gggggcatcc tgaacaactc ccacatgggc	1200
caggagatag acagtcacga ctacgtgttc cgattgagcg gagctctcat taaaggctac	1260
gaacaggatg tggggactcg gacatccttc tacggcttta ccgccttctc cctgaccag	1320
tcactcctta tattgggcaa tgggggtttc aagaacgtgc ctcttgggaa ggacgtccgc	1380
tacttgcact tcttggaagg caccggggac tatgagtggc tggaagcact gcttatgaat	1440
cagacgggtga tgtcaaaaaa ccttttcttg ttcaggcaca gacccagga agcttttcgg	1500
gaagccctgc acatggacag gtacctgttg ctgcaccag actttctccg atacatgaag	1560
aacaggtttc tgaggtctaa gaccctggat ggtgcccact ggaggatata ccgccccacc	1620
actggggccc tctgtctgt cactgccctt cagctctgtg accaggtgag tgcttatggc	1680
ttcatcactg agggccatga gcgcttttct gatcactact atgatacatc atggaagcgg	1740
ctgatctttt acataaacca tgacttcaag ctggagagag aagtctggaa gcggctacac	1800
gatgaaggga taatccggct gtaccagcgt cctgggtccg gaactgccaa agccaagaac	1860
tgaccggggc cagggtgcc atggtctcct tgctgtctcc aaggcacagg atacagtggg	1920
aatcttgaga ctctttggcc atttcccatg gctcagacta agctccaagc ccttcaggag	1980
ttccaaggga acacttgaac catggacaag actctctcaa gatggcaa at ggctaattga	2040
ggttctgaag ttcttcagta cattgctgta ggtcctgagg ccagggattt ttaattaaat	2100
ggggtgatgg gtggccaata ccacaattcc tgctgaaaaa cactcttcca gtccaaaagc	2160
ttcttgatac agaaaaaaga gcctggattt acagaaacat atagatctgg tttgaattcc	2220
aggatcgagt ttacagttgt gaaatcttga aggtattact taacttcaact acagattgtc	2280
tagaagacct ttctaggagt tatctgattc tagaagggtc tatacttgtc cttgtcttta	2340
agctatttga caactctacg tgttgtagaa mactgataat aatacaa atg attgttgtcc	2400
atggaaaggc aaataaattt tctacagtga aaaaaa	2437

<210> 78
 <211> 582
 <212> DNA

<213> Human

<400> 78

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ttccagatca aattattatt tatttcaata agactattgc gaggcattaa aaaaactaaa      60
tagtaaatatt acaaaatcta tataacttgca catttagtat ttgtcaatgt gccagagggt      120
ttcttcatga aatttgactt ctttgaagtg aaggcttttt tctatcatct cttatagctc      180
tgactgaata agtcttaatg ctttcttcat gttttctatc aataggggta aatcccgagg      240
cttatatgtg tacaatctgt tagagtatct tcagctatg tcagctctaa ctgttaaaga      300
agggcttaca aacatgattc taggcacata ttgccatca ggtgataaat tcttatcagt      360
ggtttcatgc ataaggttta gcatgatgaa cttattctga gccatttctt gtatttcttc      420
attttgggca aatactttct ttagtgcttg agagtattga caatcctcca ggtgatgaat      480
aaccattaat ggcttcttac tttttgagc ataaaagaga ccttgctcat aagtttgtac      540
ccaagagatg gcatctaccc atcctcttga gagtgactga gg                          582

```

<210> 79

<211> 511

<212> DNA

<213> Human

<400> 79

```

ttgaaagcct ttacatttat tgaagagcgg acatatgttt gcaaatacaca gtgtgcatgg      60
gcatgcatta catggttcat aatgctattc caattaggct ttcatagtgt ctttctcata      120
acgtccttta aaaaaaataa taactgaaag ggaaaagaaa gtgtcaattg caattacatt      180
tacaaaacca aactgctgct ttcaattaga gtgaatctgt gcttgcgtac tcagatatac      240
acatgtagat ttccaaggc ccatgcacac acttctgtag gggcagaaat tttctatgaa      300
taatggcttt agcaaccoga atagtatctc taaacattga caagcttggg gaacagggca      360
acaagtgcaa tgaacaatac aatttctaac gtttgtccca gtcaacatac cactttgccc      420
tgagatatt taacacagca ttcatTTTTT ggaatgataa gggataattc atctaattaa      480
gggtattata cagaatatac ctataaaaga c                                  511

```

<210> 80

<211> 987

<212> DNA

<213> Human

<400> 80

```

gtgatgatcg acatttgaat ctctttgccc ttccaacgg ctatggcatc aggttctaaa      60
ataagctcgt aatttttcct gttattttta taatatggaa atattagcat agtgtttctt      120

```

```

ttgatagtga tagactataa tccatattta aattttatag agaagaaatt ttattgtact 180
gtgatgtaga tatttattat ccaggtaagg atttgcccgg tgtgtatttt ttacaattga 240
gacattttac tttaatcttt aacaaaaaat gcattaaaaa cactctcaa aaaaaacaaa 300
aaaaaaaaaa aaagacaacc caaacggggg gggaaaaaag aggtgattgg caccctttat 360
cacgaaaatc ttcctgcggg cggccctcta ataaccagtc ttctggaaca actgtgccca 420
aaccgaggtg tcgctcttta aaataggcgt ggtctccac catatctaac actcaaattg 480
cgccgcctct tctcaaaaga acccacaat atgtgtgccg accaagagtt aaaaaaccg 540
ccttgcgttg gacggggcgg acattatctt ggattggcac caacactatt aaaagaggcg 600
atgcgacacc caacccgat taattggcag cagacagaaa tcctttctca actagtatag 660
aaaactgttg tggccctcca ccacacaaa ggacgaatcc tacccaacta atgtattagc 720
tcctctccag tgtgaacaat atactaatct ggatgcgcc acaccaagc tggttagcta 780
acacaaacac caggaggga agacacacgc attttgtaac acaaatagat ctaatattag 840
actcgtgccg tataacatcg gacactaatc tctagcacca gggggcgtcg actgtaatta 900
tgtcccgcca ctgctgctgt tcgtcggcat gttatcatgc ccacgctct ctgtgatcct 960
acacgagagg gatcacccca cgcttat 987

```

<210> 81
<211> 483
<212> DNA
<213> Human

```

<400> 81
ctgttcaaaa aaggttttat ccaaaaaagt taatcaagac aagcaacaga tactgcaaag 60
cattatatac agcaccatag tccaggggcc aaagaaatca ggaggggctg ggcagtagag 120
gaattccata tattaatgaa tgtgagatta agtatagagt gaagacatta acacacaatt 180
ctaatttctg ttaggcagaa tgcctcccta ccctgatgcc acagcctttc acgtttccta 240
aaccctagta acctctgac tccatctgcc tcatcaacac gtcaccaccc tttgctcttc 300
ttccaattag tcacatgttg gctgaattta tttcactcca gtactttagg accttgacag 360
acaaatcgat tacaaggtea attcccagga tttcttcagg gtgtgttcag gagtgcagat 420
gttctttgga tgacctttct actaaattag acctctgaag gagaaagcta cttgccagag 480
gct 483

```

<210> 82
<211> 552
<212> DNA

<213> Human

<400> 82

```

tttttttacc acctagaaat aaacattata ttttcctctg atatgtaggt aagaacttca      60
aatataagac ataattttaa agttttataat tgacatagtc agggattata aataatatca    120
cacaaaaata gctcttaatg caagaaatga atctccagga tagatcatac taatctatcc    180
aatccagccc tctgttctga aagcagcaca tgaaaaggca gagaaagaaa aataatctct    240
acgacctggc ctgttaaaca tgtattttatt tcctgagtaa ctattagggtg ctagctgtaa    300
tgggctattc agtggaggac agtgggtcaaa gcctcttatg atgtatggca gatgccagaa    360
agatatgaaa gatgtgatgg tacaaaaaag gaagttggag tcacatccag ccacaggact    420
aactaagcct ctttggggca ggagactttg gaagtgttga aggagagtag aatctattca    480
gaaagaaaca actgggggca ggtccttcca gtctgaatga agattaacta ggcgtaatgt    540
aactggcatc at                                                                552

```

<210> 83

<211> 505

<212> DNA

<213> Human

<400> 83

```

gactgtagaa ggaaagcatt ttattgcaaa taactaatag ttacaaaagc acttttttaa      60
tgttattatt agatgttaag ccgaaaatct agaaactaac atttaccag gttacaaaat    120
aagagcttca tatttttcaa agtctctaag ggtaagggtac atccccagat aaaatgagta    180
taggccagtc tcctttggct ttgtggattc tttccaaaaa ttttccagac tatttagctt    240
tccttgtgta gttacagctc aaattagaaa ctgaagaaac agcaagtggc caggcagggt    300
agaaagcaaa taaactgagc tacctgtgcc tttttccaaa tcagtatatg tgcttggctc    360
ctgaaaaaaa aaattctgat atgtaggcac tctcattact tagtgagata ttagtgaaga    420
cctttcaacg tataacacac agtaactgtt gcatagtttt aataaacact tgaattttcc    480
aggaatgtga ctgctgtgta aatca                                              505

```

<210> 84

<211> 671

<212> DNA

<213> Human

<400> 84

```

gcggccgcgg ctgcggcggc agcagcactg gctgggtctg gctgcacagc aatggggctg      60
atcatgtgct ccaactgtgt gatttttgcca tcttcaatca ttttaggggc tggagctgct    120

```

ggaaacatgg aatactgagc cccaatggca gggatggcta ctgtaccagg tttaatggca 180
 actgggttga cggtagggat ttccaaattc ggcaccagtt catatccttt ttcttgotgc 240
 tttcctttcc cttcatgata tcggctatat ataccacggc cagcagaata tccccgagg 300
 taggaacccc taggccttg ggctctgttg ccagctgcac ctgcacctcg gcctcttatg 360
 ctgcctgctt tcacaaagta gtccctgttg ggcccaatga gcgcgttgta ggggtagccg 420
 tagtaggcca gtgtgtaggg gtgcaggag tacacgtagc tgggctgctg cgctgcctca 480
 gccgcgccgc cgcccttggc tgccttcttg tagcgcgagt actgctcctt gtccacgggc 540
 ttggccagcg tgacctccag gcacgagccc tccagctcag tgccggttga gttgttcatg 600
 gcatgcacgg catcctcgcg gctggtgaag tgcacggagg cgtagggtccg gatcttcttg 660
 acgcgctcca c 671

<210> 85
 <211> 563
 <212> DNA
 <213> Human

<400> 85
 tttttttttt atatctgtta taagcttttt ctttttttaga atttaagctt atgagtttat 60
 ctacgcccac tatattcata attacagttt tatactctgca tacaaaagct atgtaaaaat 120
 ccatttttcc caaatataca aatttttttt ggatagttaa aaacattttg atcacagatt 180
 tcaacagagt tttaggctga aaaaaatata accatctagc aatatcactt aacactgttt 240
 gcaaaacaca aatcttccaa tgactgtaaa tcttttttcta ttctgtagta tttttctgat 300
 tctcagggca tgaaaacatt atggggaaaa aaaggatttt ctacgaagaa agcatggaga 360
 actaatttgg ctctatggtc aaattaaaaa tgccaagtta ataagggaga accaaaagaa 420
 agaagtggca taatgtcaca tcagctcatt catgccctga taatttctgt atcaacaata 480
 catatgtaaa gtgtctcctt ttgtcttaca ttgtgctcca taatttacat gagtattatc 540
 tgcctcctga ggaggacaga ttt 563

<210> 86
 <211> 545
 <212> DNA
 <213> Human

<400> 86
 ttattagga ttcctgccac cttattaaca tataaaacaa tctggatggt gacatagaaa 60
 tgcaaatttc actatacaaa ggtaaggctc caagcacagt aacatggccc ccatatcttt 120
 agtatttcaa tgaaataaac ttattgggga ttcaccccgga gttgtgttta taaatattag 180

```

acaaaccaca aaatatattc caaatacata acattttaca atatttttca agcacagaca      240
aatacatact ttactttacc tacattgttt tcatgatcca acttgcattha gcactaaagg      300
caatatgttg tgtgtatatg tatttgccat atgtgtgtgt gtattatata tatttattta      360
tatccacaaa tgtacactca gtggcattta tggaaaattt aaccctttca ggctgtgggt      420
tttaccacac atagtatctg agagggagaa gaaccaataa tacatctcaa attcctcaat      480
tagggcaaaa taagcacaat tatgcatgag gggcatatat gttgtgtcta ttcaaagaca      540
cacat                                                                    545

```

```

<210> 87
<211> 464
<212> DNA
<213> Human

```

```

<220>
<221> misc_feature
<222> (28)..(28)
<223> n is a, c, g, or t

```

```

<220>
<221> misc_feature
<222> (276)..(276)
<223> n is a, c, g, or t

```

```

<220>
<221> misc_feature
<222> (422)..(422)
<223> n is a, c, g, or t

```

```

<220>
<221> misc_feature
<222> (463)..(463)
<223> n is a, c, g, or t

```

```

<400> 87
gcagcgtttg tccctgggca tgtgatgnng agtcctgggc acatcgagat gctttacttc      60
tttctttcga cctcttaaaa aactaaacca agccaaacca caaaggaaat ctgcacaact      120
taagagaaac ttgaaaggga tctgttaact actagtttgt actaagtttt tttcaagaaa      180
gggaaacaaa tttatatata tatatatata tatatatatg tgcaatatat ttttacactg      240
tgtgattaac attagggagt actgagtgca tcactntatc agtgtgacgg gtgatgtcca      300
cgtcatggct gttctgactc tgaaagccac ttctgctgat gtctaaaccg cactcaccgc      360
ggacgtccgg ggttgtggtg gccctgctgt gcctcctgca ggtgagaggt gtggtgttgc      420
cngttggact tgctgttgag cctgggttgca aacctgtagt gana                        464

```

<210> 88
 <211> 611
 <212> DNA
 <213> Human

<400> 88
 ttgtgctaaaa atttaccaaaa atagtttgaa cacataaaaa tattttttaaa aaaacagaac 60
 caaaaaccca gcataaaattt agttgtatag gcattgggta gaggacactg ttttcactaa 120
 ggattatatt caacaacttt ctcttgagtt gttactaaaa ttctgattct gaaccttata 180
 gcttataatg gtgccaaacta ttagaaatgg gaaaatctaa ttcagtccaa tgtaacatgt 240
 attatgatat aatagatgaa gggatatgtct acactataat aaaaaataaa catatttttg 300
 gttattttaaa gaccatcttc ctaacctgta actaaaataa ctgtatttga tttaaactta 360
 ttttaagtga gtgaattatg gaaagctaac ttaaagggtt gaataatcaa ttatgagtaa 420
 ggaacacctg ttgacagccc cgtgaccctt cagaaccagg catttgctga aaaaaagaaa 480
 tcactagcat tgaatatagc ccttagtcac gtgagagatt aacttcacga gcaaccagc 540
 atgtagagga tgagggtggac tttcccagcc acccactcct tgagggggaca gtagtattca 600
 tagtgaaaact g 611

<210> 89
 <211> 515
 <212> DNA
 <213> Human

<400> 89
 ttttaacagta aaattttattt ttattttttgc atatttctcaa atacacattt acaatagtat 60
 cacacttctt atatgaattc ttcatagtta ttttaagtat tttacaattt gtacagagga 120
 agggacatac aatatctaata aggctatttt tcaaccaaata aataattttat gtccttgtaa 180
 gattttgtac ctcttttaaaa ctttcaactt caacatccac ttttttagct ttgctaataca 240
 aattaagaat taaaaccagc ctgcaaataa taacagtata taacattaag cacaatttca 300
 tttctttctt tatacaaatag ttctatatatt acttgaccaa atgcttaatt acctttttaa 360
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<210> 103

<211> 388

<212> DNA

<213> Human

<400> 103

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tttttttctc ccagtcattt gattttattg tgtttttact aagcattttt attatcttca      60
tgtagtcaaa tgtgtcaata ttttggtgcc actggatatt tccaccacgt ttccttctgt    120
atttatatgg cttcattttc ttacatttgg atcctggatc cagatggagt tcattcttgc    180
atatggtgtg aagtacaggt ctaacttcaa ctttctccaa ggggctttcc agttggctca    240
gcaccattta ttaaagtctg ctttgacctg cgattgaaga tgccaccttt aactcctcat    300
ccccacccc taagaaacct cacggaacat atgaccaag agcagagcag acataaaaag    360
attaactgag ctactgagat tcggtcaa                                         388

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<210> 104
 <211> 545
 <212> DNA
 <213> Human

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<400> 104
tttcttttta ttgctaaaga gtattttatt gtaaataatat atcacaattc tttattcttt      60
ctgtcattta tgggcattta atttctttga ataaatttaa caagttgcaa atgaatattt    120
agcaaattgc actcagatta aaataacaaa ataatctctt atcagaagct aagaaataca    180
ttttcctcct cctcatccat atccaaagac ggttctgaaa atgccttttc ttctctatta    240
tagcaacacc tagtggcttg agaaggccag gtctagaggt atgcatttac ggctgggaaa    300
cactgacctt tagctttgaa gacctcaggt agcacctaga cgtcggctat aaccgcataa    360
caatgggtccc catctgaaac catttaagtc agaatctttg gaggaagagg ccaggattgg    420
taggttataa aagttgccca gatgatttta atgtgcagcc aaggctaaga gctacttata    480
tagaccagtg gtttgcaaac ttttgtcaaa taatcagaat cgcgtgtcaa acacagattg    540
ctggg                                         545

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<210> 105
 <211> 580
 <212> DNA
 <213> Human

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<400> 105
ttttttttta atgttaacat tgagagtcac tacggctaaa gotttgctt catcacatag      60
ctaaaaagaa gggtgagctg gaacttagga tactttaaag catttctgt ttaggtatta    120
ggctgataga gaatcatgtg taactggggt cagcattcct ataatttttt gagccaaaga    180
cagaatacac actttacct gacaggtttc ttccagaatt taggacagct gatgaaatga    240
aaagacacac acccaagcca agagtgc aaa aggatgtagt agcatgattc cgccaaccaa    300
atgcctcata ccctcagacg tcccaaatac agtggtgagc aggtaaattt ttaacaacaa    360

```

tctttctttg tgaggaaaaa agttcctgat ttccataatg taaatacttt cactgactgg 420
 tttgaagcca tcaacacgtc aactaacaat tggttcctgc atgtctataa gctggcctta 480
 gcacaccact gcaaacctac ttattactta tattttcaga tacattacag cacttatcaa 540
 ttctaacatt gtgaaaaact gctgtgcttt aggcaccttg 580

<210> 106
 <211> 618
 <212> DNA
 <213> Human

<400> 106
 tttttttttt ttaaagtttt acttgaata tgtgtatttg ctaaagttac aagggaat 60
 attgcaaatt atacatcatt tgaaaaatta tctctcttta gttaattttc agtcacaata 120
 ttggatgtag cagctccaaa tagaggttac ctgattattg cttttataat tgaattctta 180
 aagagtttac atcataatta tataattgta tttttaaaca tcacagaaac ccaacatgta 240
 cctatttgta atcatcagag tatatacatc tgattaggac tcagctatgt tcaaggcttc 300
 atcgagccca acatacaatt atcatttgca ttttctgcta caatcaaaga aaacacattg 360
 tgtgctatta gtggccattg caagaaggaa gatgctgttt tcaataacag gaaatcaaga 420
 acaaacaaaa taatcgtctt ccatttaaaa aaaaaagaaa gcctacagaa aagtgaag 480
 gacaggggcc taaaaacatc tagtgatgcc aataaaatgg aatgtttttt aaaaagtgat 540
 ttgtctcact gaagctgcag aagggtatcc cacacttata tattatgtga ctgcactaaa 600
 aacagacgct tttggtgc 618

<210> 107
 <211> 538
 <212> DNA
 <213> Human

<400> 107
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 ttgagaaaaa taaagacatg aaaggatagc ccaagagagt ccagtaaaaa aagcagaggc 120
 aaagttttcc ttggcttttg gttatgggct gtctgctgaa tatgagtctt ggatcttttt 180
 cagcatcaac ttgcaaaagc tatgcctttc cacccttgcc cttgtagctt ttttgagtcc 240
 aggtctcccc actcccatgc caatggaccc tttataatgg ggaaggcatc acagcaagac 300
 gcaggcttgg ggctttccca atgaccaggt tctcattaag tgccatctca ccatcaacca 360
 gcgacagcaa tgtccctttt gcccaagctc ctcccttccc tgcactctgg ttgccctcta 420

aatggcacca gcccaaacca gggacagtca ctctgtccact cacttcccaa atatattacag 480
 agcgccctgtt ggggtgccagg ctctctccagg ggccctgctg ccaggccgaa gccacagg 538

<210> 108
 <211> 542
 <212> DNA
 <213> Human

<400> 108
 gaaaaaggaa tctgtatttt atttactcat tcatatttta gatccagaac caaagaaaag 60
 caataaagtt ggtgaaagac tcatacaacc cacaatgttg ccccataaa aaatattcca 120
 aattaatttc tggccacaaa ttctattttt acagcatgta attgaaacca gattaccttt 180
 ggttttttcta agccaccccc tccacccta gagagggggc taaaaagaat gtagtataag 240
 tgaatcttga aagatatcct tggattctgc tgtctcaa at acagtttgct gcaaaaagtc 300
 ttgccaact aaactatcat taccttcccc gatgctaagg ttgaaaatca gcattcttgat 360
 tataagccta actttcaagt ttctaactca gctgcaaaat attttcccaa ctaaactgt 420
 ggtgttccaa aaatatatac tatacagcaa ttcttaaagt tataaatgtc ttggcgcatt 480
 tggcatactt gcttaattcc aaaatcatta aaaagacaca tttagtgaag aagtatctca 540
 ca 542

<210> 109
 <211> 484
 <212> DNA
 <213> Human

<400> 109
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 caggaccaa aaaagtgatt aaatTTTTTg tttgtttgtt tatcttacca aattgtaaca 120
 catgtagttt tcttctttct ctgtgttcta ttttattatt gtaaccactt tggctttttt 180
 ttttgtataa tcaattgcag ctagaatggg gtatggctct taatagatat ttgggataat 240
 gctgagtccc agaaatgtga agcctttccc gagtattgag ttcattaaag gttattatca 300
 tctgttttaa tcagtaagtg attttaactt tcttcattat cccctcctct tgtttaactg 360
 tggataagta gttcccatgg attgcttctt ctgtcttctt agcgagaaat atcgggtggct 420
 atgagatcat agctcaacag cttcaattct gtgtcttctt tctgagcaat ttttcttctt 480
 ttca 484

<210> 110
 <211> 478

<212> DNA
<213> Human

<220>
<221> misc_feature
<222> (57)..(57)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (78)..(78)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (89)..(89)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (165)..(165)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (170)..(170)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (200)..(200)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (248)..(248)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (270)..(270)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (360)..(360)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (365)..(365)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (379)..(379)
<223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (385)..(385)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (402)..(402)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (439)..(439)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (457)..(457)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (474)..(474)
 <223> n is a, c, g, or t

<400> 110
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 aaaacaaatg gagtgggnca caggaattnt cagaaatgga ggcttaggct gtccatacag 120
 gattcagcaa gtacttgggg actgcgacta gaagaagcca gggtnnggan taagtagctg 180
 aggaggagag ggagctgatn tggaggagag caagggaac ttcaagggaac aaaagggaag 240
 ctgcaagnac cagctccatt aattcagcan acattccttg totgtatgcc atgccagggt 300
 ccttgttcta tggttctctc agtggggtag ctagaaactt gcccaacaga caggaacagn 360
 cagangccaa agcaaagant tcctnaaagg tagccggcct gntgccaaac ctggggacaa 420
 actttatgga ggcgcctgnt tttagccaga ccccgantta aaccttggtc ccancctg 478

<210> 111
 <211> 313
 <212> DNA
 <213> Human

<400> 111
 tttttttttt tttttttttt ttgaggttta tgctcatttt attataaaaa aatacagaat 60
 ccaaagttga ttgtgacggg aagagggagg cccggtcgcc agctccaggc ctggcaacgc 120
 ggcccgcgcc gccgaccccc tacaaaagcc ctctgccac cccccaccac cgggcgtgcc 180
 tcgagccgcc ggccggcggt acaacaatat atatttatat ataatatata taaaacacag 240
 agtcaggaaa ggcgggtaga aatatgaaat ccgtataaat gtgttggttc cttcattaaa 300

gtgtcttcgg gga

313

<210> 112
<211> 498
<212> DNA
<213> Human

<400> 112
aacgtttttt tttttttttt ttttttgggt gtatgtatat aaactttatt ttattctctt 60
ctgggggttgt gttacatgac aagaaattga attaatcaaa taaaatttta gttcggggttg 120
cttaggtttt tactgctccc attcttgctt ttactaattt atccaagatt agatgtgatt 180
actatttaaat aataatttag tcctcacact tacaaccac ttacaatacc agcatgcttc 240
tatcactgta attctattca attctcaggc ccatgaggca tgccagccag acgaccagac 300
agcattttatt gagtgcccac tctataccag ccacaaaaga tcctgtgtca gaaggggaaa 360
caggcttgga ggcttgaggt atgtacgtga tagcctccct ccaggtccac acaactggta 420
ctgctggggc tgtaactaga actcaggcct ctgcctctca agctcaaggt cggatgtcca 480
tgtgcttctc acgttgcc 498

<210> 113
<211> 590
<212> DNA
<213> Human

<220>
<221> misc_feature
<222> (450)..(450)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (515)..(515)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (547)..(547)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (558)..(558)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (570)..(570)
<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (581)..(581)

<223> n is a, c, g, or t

<400> 113

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tctttatcag ggagggggga aagtacaaaa ttatgtccct gatatgattc aaccatgtaa	120
aatgatgtac atttatgaac gacgactaga agtgaacatg aataactgaa aacaaacagt	180
gtgatgcaag tgaatttttg gagggtgaga tggtcattat attgttcttc gagcaattaa	240
atattttatt ttcttcccaa aacaatgtcc acaagggggc agacagaaga tgacaaataa	300
aaccatttaa taaaaacctc agctgaaaag ctaataactc cagaatgcag gttgaaagca	360
agcttaaagg tcatctaggc tggggtcagt agctcacgcc tgcaatccca acaccctggg	420
aggcccaggt gagaggaccg ctcgagcccn ggaggtaaag gccgcagcga gctatgaccg	480
cgccactgca caccagcctg tgccacaaag taganttcgt cccaaaaaaa aaaaatcctc	540
ctagtcntct agtccatntc cccccctggn caagaaggac ngaggcccca	590

<210> 114

<211> 365

<212> DNA

<213> Human

<400> 114

taaaaattctt tggatttttt attggattca cataaagcaa agaacttact cacttggacc	60
gagaatatat tgtaatgttc cataagtcac aacttaagga ccgagaatat attgcaatgt	120
tccataagtc ataatttaat gtgcagtaag aacccatgaa gttgtctgac caaaagtaac	180
actcttctgt tgggaaagat ttacatcct tttattcttg atgaatcctg aattctagat	240
gttgggttta atgcttcaca caatggcaca ttacaagag gtacaaaaca cttattgagc	300
tttcagggcc actgtaagg gcttgcagaa tagcctcttt gcaaccaga gaattaatct	360
gattc	365

<210> 115

<211> 539

<212> DNA

<213> Human

<220>

<221> misc_feature

<222> (359)..(359)

<223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (481)..(481)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (483)..(483)
 <223> n is a, c, g, or t

<400> 115
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 ttctggtgga ttaagtgtctg cttaaatact aagactatcc attcaactttt gcctcacgcc 120
 tctctactaa actgcagctc agttctgcct ctcataatat gtatgttgag taacattatg 180
 accacacagt gctcatcaaa aactattgct ccagctgtaa ttttaaagtgt tggaggtggt 240
 tcaaaattct aaagagttat agaaataaca cacatttgac aaatacatat aaaaatagtt 300
 ataacatatt gaaatcacat taaaatatga aaaaccacaa aagcataatt gcatcatant 360
 atttgtgttg ctagacactg tccatctatt tttagaaaac gtcttaaatg tcactcaatg 420
 gggcaacttt cctggtttcc tatgtcttac cttagaagca agcagtgtgt tagaatggat 480
 ntncatgca cgttagaccc caagatacaa caagcttctc tatacagaag ccatccatg 539

<210> 116
 <211> 602
 <212> DNA
 <213> Human

<220>
 <221> misc_feature
 <222> (294)..(294)
 <223> n is a, c, g, or t

<400> 116
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 taaaacttca ccacatattt tcagctaagg taaatctgct tgggtccaaac aaaacaaaac 120
 aaaacaaaac accagactgc aacaataaca ggaaaagatc ctcttcagtg atttatgttg 180
 ttctcttact ttcataacta gtttgaatgc aaggctggta aagggataca cagagaatca 240
 ttatttttaa taacaaaagc cattcaaac tctctctacc tgtcaaggat gttntatgct 300
 cccattotta tttgtttggc agtaaacata ccttgcccac agtcgccagc atcaaacca 360
 caggacaaga cattgcatgc ttggtcacag aacttatcag cgagccagga attcgcacat 420
 ccctgattac agtaagagac actgtttatt cctccaccaa actgccaggy ctgtccaact 480
 ccaatactcc cagtacctcc acctcctgca atatagcgac tccctccact gtttccagag 540

caatccccac catcccaatc gcaggctgaa ttatttacag ccttgtcaca atagccatcc 600
 tt 602

<210> 117
 <211> 351
 <212> DNA
 <213> Human

<220>
 <221> misc_feature
 <222> (341)..(341)
 <223> n is a, c, g, or t

<400> 117
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 tgcgcagtggt tctcgtcatc atcggccagg actcacagtg cccgcggcag aggcctccct 120
 agacctccct cccgtccagc ctcacccgct gcctactctc ctcacgcccc tgctccaggt 180
 cccctggccc catttcgctc gccacgtttt cataatcctc tcaggctccg ggcaagcggc 240
 gccgcccgc atgggacctg atcatataag gaaaatactg cgggctcatc cgggggctgc 300
 aatggtaacc cgaaagcgcc ctaggctact acaatcacccg naccccaact g 351

<210> 118
 <211> 462
 <212> DNA
 <213> Human

<400> 118
 gctaagaaat aactttttatt aaaaatactg tgctagtact tatgcaatta cataatttta 60
 actaaatatt gtccactgcc acaattcgca ttaccaaact catattacca aatttttaggc 120
 cttgatagag cctaaatgct tcagtcactt cagaccaata acttaattct gttttcacat 180
 accttataca ctggcctacc aatagctctc aattcctgtc aatactttcc ccattctgca 240
 aaaagagggc cccatcccca tccctaataca aaaccaatgt gttgtacctg aaactgcaaa 300
 gattaatgct tttcgatgac cactaacttt tgaagccga aggcctaact tttagacaac 360
 taaagctaca cactgttaaa attcttgggc ttctgtctta ttcagcaagc tgactcagta 420
 aaattaatac actgtatgaa aaaagctaac atacctacaa tc 462

<210> 119
 <211> 332
 <212> DNA
 <213> Human

```

<400> 119
tttttttttt tttttttttt ttttggttta aaaataaatt tttttatta catgataata      60
ttgacagttt acataaacia agttattttag tgtatgcaaa gcaactataa aatacatttt      120
gaaaagatat aaaaatcttt gaaattcttt cttgatatca gatctaccaa atttcgagag      180
ccaccattga ttttttagga tcaaaacaaa atggcttgag agattttggt ggtcagccaa      240
actcagtcca ggaaaaaaga aacattaaag cattgttttg tgtttttaaa agctctaatt      300
gataatttatt ccaagctcct ttogtatoga ag                                     332

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```

<210> 120
<211> 473
<212> DNA
<213> Human

```

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<220>
<221> misc_feature
<222> (373)..(373)
<223> n is a, c, g, or t

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<220>
<221> misc_feature
<222> (429)..(429)
<223> n is a, c, g, or t

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<400> 120
ttttttttta aatttcttcc agtttgggat tgtgtatata caaaaagctc aaaataaagc      60
aactctgcaa tataatctta aaataatggc tactggggga aattctatca caaccattga      120
aaataatggt gacttctcac ggagtctgtg gcatctgaga acccagttta ttaaccaaag      180
tcttgctcat attagcctca gttaccaga ttaaagcagg aactccggcc ttccctggac      240
tgctgaaaac ccaacagatt ttctcaacat gctataagga aagagggaaa aattggtttc      300
agctcacacc tcatgggctg ggaagcttct gggaaggcct ccaggccagt ggcacactcc      360
ccaactttat ggntaaaagg aggggccaat tttcattccc cacaggcatt cacaaggagt      420
tcccaccnt ccaaccacac agtggttttg gacaccaagg ttcacccttt cct              473

```

```

<210> 121
<211> 525
<212> DNA
<213> Human

```

```

<400> 121
gagaggatgat ataatttatt tttcttttcc atccaaatta tcagtaacag tggctaaatg      60
gcaagatagg ctaaaaaact ctaagtgacc caattttaca aattaaagaa gtaagtaaac      120
attagaatga atacagttaa acaggagagg ctgggcacag tggctcacac ctgtaatccc      180

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agtattatcc agtaaaagtt tagcaagcaa attcaaagaa gtctgttggtg caaccatagc      240
cctttgcagt agaatctgct atacagccta ttatgaggga tcaatttctt tctttcttct      300
tttttttttg agacagagtc ttgctctggt gcccaacctg gaatgcagtg gggatgacctt      360
ggctcactgc aacctctgcc tcccagggtc aagcaattct cctgtctcag cctcccagagt      420
agctggatta caggtgtgca ccatcacacc cagctaattt ttgtattttt agtagagatg      480
gggtttcacc acattgggtca ggctgggtct aaactcctga cctca                      525

```

```

<210> 122
<211> 849
<212> DNA
<213> Human

```

```

<220>
<221> misc_feature
<222> (598)..(598)
<223> n is a, c, g, or t

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<400> 122
atatgtatat ttccctctga ttttatgact gatttacaaa ttaggagtgc aaatgggctg      60
ttccccgata gcatcttctg ggaagaatcc aaccaagata caaagcagat gatgggtggat      120
cggcaaaactc ttttctatga aaagaaaaac cagatatacc agggactgga aagcacctgc      180
ttgaaaattg atatgagcat gtctgaattt ttcccttata agagcctgag tattgtaaca      240
ggctctcttg acaggggggt gaaaaataaa aaaagaagtt aacataatta aaatgcttgg      300
acaaaacatt tgctttatat agattcttac aagtaatatt tgattaggta tcaaaatagg      360
tttaggcagg tggaagttct gaatttcaag gcaaataagg catgaagggt ggaacattgc      420
atctagggaa aataagagaa ataagtgaag gtctgaccct acattgccaa ttctcagacc      480
aagtacaaag tattaggaat tttttatata agctgacata tttgtgctta cagtaaagcc      540
atattagatg cacacatagt gactttatta aatcaaataa gtgtgcagag cagagcanat      600
ctaattaggc tttctctttt agagttttct tattttactc ttattagctc cctccagttg      660
gtcatcaatt tcctatccta catcagatat ttacactata agattctttg gtttaaaatc      720
ctcttcoggt ttacatttta atttctgggg cgctaaacac atacttctgt cccggtctta      780
tcctcttatt ggaattcccc acagcgtggg caaaaacgog ggctcgaaaa atggggggcc      840
ccttccctt                                     849

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<210> 123
<211> 454

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<212> DNA
<213> Human

<220>
<221> misc_feature
<222> (433)..(433)
<223> n is a, c, g, or t

<400> 123
 ttgtgagcaa catcggctgt ttattcactt gtgtgtgagt gggctgagtc cgagaaaggg 60
 gtcagcaaaa ggtgggtgga ttatcattgg ttcttatagg tttgggatag gcggtgtagt 120
 caggagcaat tttttacagg caggggatgg atattacaaa gtacattctc aaggggtgggg 180
 aggatgttac aaagtacatt cacaagggca gggaggggtgt atcgtcacaa gggcagggag 240
 gatgtattgt cacaaggggtg gggaggaatg ttacaaagta cattcacaag gacaggagta 300
 tcacaaagta cattatcaca aggggtggggg aatgtcaccg tggcttgacc attagtgcag 360
 ccagctccag aggaccttac caaaaagttt ccatacttgc acgtgttttc ctggtggcca 420
 aaaatataaa acntttaatt tctgggattc cttt 454

<210> 124
<211> 485
<212> DNA
<213> Human

<400> 124
 ttcagatttg acatgtcaat ctttatttaa gacaacaaaa gtttgtacac tctcatatta 60
 agatatatatt cttttctagt catattaaaa taatctcatt ttgttactca aaaagaatac 120
 atagggaaga gaatgaacat aattcaagta gatagatttc taattgggta aaacagggtt 180
 aaacaaatga tgttcaaaat atacttatta aagggaacag cacctagaaa taggcagtag 240
 ggcaatgttc actttaagaa ttttatcaat aactagggca aagaacaaaa tcattatcaa 300
 attttgaatt acacaaaagc aatggcctat taccttggtta acatttgata tttctatata 360
 tcttcttctc tagttgaaat gggtaatgac ttgtattaca aggatgttac acattctaaa 420
 atgatttaag ccaaaaagatt atctttaata cattacttct agatataata tgtacttgat 480
 gtctg 485

<210> 125
<211> 558
<212> DNA
<213> Human

<400> 125
 ttttcagaca tgacagcatt tgacacactc ctttttaatt tattgcagaa ataatatgaa 60

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catctgggaa aatgatagtg ctaaatatct cgtgaagtaa gtcattctta gaaagggatt    120
tgtgactttg aagtaatata taattagcaa gatttttaaaa attattctta tgtactgaaa    180
ctcaaaacag actagcaaag tacctccaaa aaaaaaacta tcaaattaaa ctagaaaagt    240
atttccaaaa taaagacgac caaaaactag cctgagaata ctagttttct gttgctacaa    300
cacattacca caaacttagt ggcttaaaca caaatctatt atcttacagt tctgcagatt    360
agagggtccaa cacaggcttc actgggctaa aatcaagggtg ttggcagggc tgcgttcctt    420
ctggggaggct atggggaagt ttctgtttcc ttccagttct caattctacc ggctgcctgc    480
aactccctgg cttatggccc cttcctccat cttcaaagcc aggaatgggtg catccctctc    540
taagcgttct ccctattt                                     558

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<210> 126
<211> 508
<212> PRT
<213> Human

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<400> 126

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```

Met Gln Arg Leu Leu Thr Pro Val Lys Arg Ile Leu Gln Leu Thr Arg
1           5           10          15

```

```

Ala Val Gln Glu Thr Ser Leu Thr Pro Ala Arg Leu Leu Pro Val Ala
          20           25           30

```

```

His Gln Arg Phe Ser Thr Ala Ser Ala Val Pro Leu Ala Lys Thr Asp
          35           40           45

```

```

Thr Trp Pro Lys Asp Val Gly Ile Leu Ala Leu Glu Val Tyr Phe Pro
          50           55           60

```

```

Ala Gln Tyr Val Asp Gln Thr Asp Leu Glu Lys Tyr Asn Asn Val Glu
65           70           75           80

```

```

Ala Gly Lys Tyr Thr Val Gly Leu Gly Gln Thr Arg Met Gly Phe Cys
          85           90           95

```

```

Ser Val Gln Glu Asp Ile Asn Ser Leu Cys Leu Thr Val Val Gln Arg
          100          105          110

```

```

Leu Met Glu Arg Ile Gln Leu Pro Trp Asp Ser Val Gly Arg Leu Glu
          115          120          125

```

Val Gly Thr Glu Thr Ile Ile Asp Lys Ser Lys Ala Val Lys Thr Val
 130 135 140

Leu Met Glu Leu Phe Gln Asp Ser Gly Asn Thr Asp Ile Glu Gly Ile
 145 150 155 160

Asp Thr Thr Asn Ala Cys Tyr Gly Gly Thr Ala Ser Leu Phe Asn Ala
 165 170 175

Ala Asn Trp Met Glu Ser Ser Ser Trp Asp Gly Arg Tyr Ala Met Val
 180 185 190

Val Cys Gly Asp Ile Ala Val Tyr Pro Ser Gly Asn Ala Arg Pro Thr
 195 200 205

Gly Gly Ala Gly Ala Val Ala Met Leu Ile Gly Pro Lys Ala Pro Leu
 210 215 220

Ala Leu Glu Arg Gly Leu Arg Gly Thr His Met Glu Asn Val Tyr Asp
 225 230 235 240

Phe Tyr Lys Pro Asn Leu Ala Ser Glu Tyr Pro Ile Val Asp Gly Lys
 245 250 255

Leu Ser Ile Gln Cys Tyr Leu Arg Ala Leu Asp Arg Cys Tyr Thr Ser
 260 265 270

Tyr Arg Lys Lys Ile Gln Asn Gln Trp Lys Gln Ala Gly Ser Asp Arg
 275 280 285

Pro Phe Thr Leu Asp Asp Leu Gln Tyr Met Ile Phe His Thr Pro Phe
 290 295 300

Cys Lys Met Val Gln Lys Ser Leu Ala Arg Leu Met Phe Asn Asp Phe
 305 310 315 320

Leu Ser Ala Ser Ser Asp Thr Gln Thr Ser Leu Tyr Lys Gly Leu Glu
 325 330 335

Ala Phe Gly Gly Leu Lys Leu Glu Asp Thr Tyr Thr Asn Lys Asp Leu
 340 345 350

Asp Lys Ala Leu Leu Lys Ala Ser Gln Asp Met Phe Asp Lys Lys Thr
 355 360 365

Lys Ala Ser Leu Tyr Leu Ser Thr His Asn Gly Asn Met Tyr Thr Ser
 370 375 380

Ser Leu Tyr Gly Cys Leu Ala Ser Leu Leu Ser His His Ser Ala Gln
 385 390 395 400

Glu Leu Ala Gly Ser Arg Ile Gly Ala Phe Ser Tyr Gly Ser Gly Leu
 405 410 415

Ala Ala Ser Phe Phe Ser Phe Arg Val Ser Gln Asp Ala Ala Pro Gly
 420 425 430

Ser Pro Leu Asp Lys Leu Val Ser Ser Thr Ser Asp Leu Pro Lys Arg
 435 440 445

Leu Ala Ser Arg Lys Cys Val Ser Pro Glu Glu Phe Thr Glu Ile Met
 450 455 460

Asn Gln Arg Glu Gln Phe Tyr His Lys Val Asn Phe Ser Pro Pro Gly
 465 470 475 480

Asp Thr Asn Ser Leu Phe Pro Gly Thr Trp Tyr Leu Glu Arg Val Asp
 485 490 495

Glu Gln His Arg Arg Lys Tyr Ala Arg Arg Pro Val
 500 505

<210> 127
 <211> 396
 <212> PRT
 <213> Human

<400> 127

Met Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val
 1 5 10 15

Leu Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys
 20 25 30

Phe Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu
 35 40 45

Val Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys
 50 55 60

Gln Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu
 65 70 75 80

Asp Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp
 85 90 95

His Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe
 100 105 110

His His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr
 115 120 125

Thr Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe
 130 135 140

Ile Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala
 145 150 155 160

Leu Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile
 165 170 175

Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu
 180 185 190

Asp Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Ser Phe Asp
 195 200 205

Val Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His
 210 215 220

Gly Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser
 225 230 235 240

Lys Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser
 245 250 255

Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys
 260 265 270

Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln
 275 280 285

Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp
 290 295 300

Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr
305 310 315 320

His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His
325 330 335

Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val
340 345 350

Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala
355 360 365

Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn
370 375 380

Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg
385 390 395

<210> 128
<211> 219
<212> PRT
<213> Human

<400> 128

Met Ala Asp Lys Ala Lys Pro Ala Lys Ala Ala Asn Arg Thr Pro Pro
1 5 10 15

Lys Ser Pro Gly Asp Pro Ser Lys Asp Arg Ala Ala Lys Arg Leu Ser
20 25 30

Leu Glu Ser Glu Gly Ala Gly Glu Gly Ala Ala Ala Ser Pro Glu Leu
35 40 45

Ser Ala Leu Glu Glu Ala Phe Arg Arg Phe Ala Val His Gly Asp Ala
50 55 60

Arg Ala Thr Gly Arg Glu Met His Gly Lys Asn Trp Ser Lys Leu Cys
65 70 75 80

Lys Asp Cys Gln Val Ile Asp Gly Arg Asn Val Thr Val Thr Asp Val
85 90 95

Asp Ile Val Phe Ser Lys Ile Lys Gly Lys Ser Cys Arg Thr Ile Thr
100 105 110

Phe Glu Gln Phe Gln Glu Ala Leu Glu Glu Leu Ala Lys Lys Arg Phe
 115 120 125

Lys Asp Lys Ser Ser Glu Glu Ala Val Arg Glu Val His Arg Leu Ile
 130 135 140

Glu Gly Lys Ala Pro Ile Ile Ser Gly Val Thr Lys Ala Ile Ser Ser
 145 150 155 160

Pro Thr Val Ser Arg Leu Thr Asp Thr Thr Lys Phe Thr Gly Ser His
 165 170 175

Lys Glu Arg Phe Asp Pro Ser Gly Lys Gly Lys Gly Lys Ala Gly Arg
 180 185 190

Val Asp Leu Val Asp Glu Ser Gly Tyr Val Ser Gly Tyr Lys His Ala
 195 200 205

Gly Thr Tyr Asp Gln Lys Val Gln Gly Gly Lys
 210 215

<210> 129
 <211> 384
 <212> PRT
 <213> Human

<400> 129

Met Asp Cys Ser Asn Gly Ser Ala Glu Cys Thr Gly Glu Gly Gly Ser
 1 5 10 15

Lys Glu Val Val Gly Thr Phe Lys Ala Lys Asp Leu Ile Val Thr Pro
 20 25 30

Ala Thr Ile Leu Lys Glu Lys Pro Asp Pro Asn Asn Leu Val Phe Gly
 35 40 45

Thr Val Phe Thr Asp His Met Leu Thr Val Glu Trp Ser Ser Glu Phe
 50 55 60

Gly Trp Glu Lys Pro His Ile Lys Pro Leu Gln Asn Leu Ser Leu His
 65 70 75 80

Pro Gly Ser Ser Ala Leu His Tyr Ala Val Glu Leu Phe Glu Gly Leu
 85 90 95

Lys Ala Phe Arg Gly Val Asp Asn Lys Ile Arg Leu Phe Gln Pro Asn
 100 105 110

Leu Asn Met Asp Arg Met Tyr Arg Ser Ala Val Arg Ala Thr Leu Pro
 115 120 125

Val Phe Asp Lys Glu Glu Leu Leu Glu Cys Ile Gln Gln Leu Val Lys
 130 135 140

Leu Asp Gln Glu Trp Val Pro Tyr Ser Thr Ser Ala Ser Leu Tyr Ile
 145 150 155 160

Arg Pro Ala Phe Ile Gly Thr Glu Pro Ser Leu Gly Val Lys Lys Pro
 165 170 175

Thr Lys Ala Leu Leu Phe Val Leu Leu Ser Pro Val Gly Pro Tyr Phe
 180 185 190

Ser Ser Gly Thr Phe Asn Pro Val Ser Leu Trp Ala Asn Pro Lys Tyr
 195 200 205

Val Arg Ala Trp Lys Gly Gly Thr Gly Asp Cys Lys Met Gly Gly Asn
 210 215 220

Tyr Gly Ser Ser Leu Phe Ala Gln Cys Glu Asp Val Asp Asn Gly Cys
 225 230 235 240

Gln Gln Val Leu Trp Leu Tyr Gly Arg Asp His Gln Ile Thr Glu Val
 245 250 255

Gly Thr Met Asn Leu Phe Leu Tyr Trp Ile Asn Glu Asp Gly Glu Glu
 260 265 270

Glu Leu Ala Thr Pro Pro Leu Asp Gly Ile Ile Leu Pro Gly Val Thr
 275 280 285

Arg Arg Cys Ile Leu Asp Leu Ala His Gln Trp Gly Glu Phe Lys Val
 290 295 300

Ser Glu Arg Tyr Leu Thr Met Asp Asp Leu Thr Thr Ala Leu Glu Gly
 305 310 315 320

Asn Arg Val Arg Glu Met Phe Ser Ser Gly Thr Ala Cys Val Val Cys

325

330

335

Pro Val Ser Asp Ile Leu Tyr Lys Gly Glu Thr Ile His Ile Pro Thr
 340 345 350

Met Glu Asn Gly Pro Lys Leu Ala Ser Arg Ile Leu Ser Lys Leu Thr
 355 360 365

Asp Ile Gln Tyr Gly Arg Glu Glu Ser Asp Trp Thr Ile Val Leu Ser
 370 375 380

<210> 130
 <211> 158
 <212> PRT
 <213> Human

<400> 130

Met Ser His Gly Lys Gly Thr Asp Met Leu Pro Glu Ile Ala Ala Ala
 1 5 10 15

Val Gly Phe Leu Ser Ser Leu Leu Arg Thr Arg Gly Cys Val Ser Glu
 20 25 30

Gln Arg Leu Lys Val Phe Ser Gly Ala Leu Gln Glu Ala Leu Thr Glu
 35 40 45

His Tyr Lys His His Trp Phe Pro Glu Lys Pro Ser Lys Gly Ser Gly
 50 55 60

Tyr Arg Cys Ile Arg Ile Asn His Lys Met Asp Pro Ile Ile Ser Arg
 65 70 75 80

Val Ala Ser Gln Ile Gly Leu Ser Gln Pro Gln Leu His Gln Leu Leu
 85 90 95

Pro Ser Glu Leu Thr Leu Trp Val Asp Pro Tyr Glu Val Ser Tyr Arg
 100 105 110

Ile Gly Glu Asp Gly Ser Ile Cys Val Leu Tyr Glu Glu Ala Pro Leu
 115 120 125

Ala Ala Ser Cys Gly Leu Leu Thr Cys Lys Asn Gln Val Leu Leu Gly
 130 135 140

Arg Ser Ser Pro Ser Lys Asn Tyr Val Met Ala Val Ser Ser

145

150

155

<210> 131
 <211> 344
 <212> PRT
 <213> Human

<400> 131

Met Gly Pro Pro Ser Ala Pro Pro Cys Arg Leu His Val Pro Trp Lys
 1 5 10 15

Glu Val Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
 20 25 30

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
 35 40 45

Lys Glu Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Arg Ile Gly
 50 55 60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser Leu Ile Val
 65 70 75 80

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
 85 90 95

Gly Arg Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val
 100 105 110

Thr Gln Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp
 115 120 125

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu
 130 135 140

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
 145 150 155 160

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Val Gln Asn Thr Thr Tyr
 165 170 175

Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
 180 185 190

Leu Ser Asn Gly Asn Met Thr Leu Thr Leu Leu Ser Val Lys Arg Asn

195 200 205
 Asp Ala Gly Ser Tyr Glu Cys Glu Ile Gln Asn Pro Ala Ser Ala Asn
 210 215 220
 Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Val Pro
 225 230 235 240
 Thr Ile Ser Pro Ser Lys Ala Asn Tyr Arg Pro Gly Glu Asn Leu Asn
 245 250 255
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
 260 265 270
 Ile Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
 290 295 300
 Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Met Ile Thr Val Ser Gly
 305 310 315 320
 Ser Ala Pro Val Leu Ser Ala Val Ala Thr Val Gly Ile Thr Ile Gly
 325 330 335
 Val Leu Ala Arg Val Ala Leu Ile
 340

 <210> 132
 <211> 479
 <212> PRT
 <213> Human

 <400> 132
 Met Lys Ser Gln Gly Gln His Trp Tyr Ser Ser Ser Asp Lys Asn Cys
 1 5 10 15
 Lys Val Ser Phe Arg Glu Lys Leu Leu Ile Ile Asp Ser Asn Leu Gly
 20 25 30
 Val Gln Asp Val Glu Asn Leu Lys Phe Leu Cys Ile Gly Leu Val Pro
 35 40 45
 Asn Lys Lys Leu Glu Lys Ser Ser Ser Ala Ser Asp Val Phe Glu His

50		55		60
Leu Leu Ala Glu Asp	Leu Leu Ser Glu Glu Asp	Pro Phe Phe Leu Ala		
65	70	75	80	
Glu Leu Leu Tyr Ile	Ile Arg Gln Lys Lys	Leu Leu Gln His Leu Asn		
	85	90	95	
Cys Thr Lys Glu Glu Val	Glu Arg Leu Leu Pro Thr Arg	Gln Arg Val		
	100	105	110	
Ser Leu Phe Arg Asn	Leu Leu Tyr Glu Leu Ser Glu Gly	Ile Asp Ser		
	115	120	125	
Glu Asn Leu Lys Asp Met	Ile Phe Leu Leu Lys Asp	Ser Leu Pro Lys		
	130	135	140	
Thr Glu Met Thr Ser	Leu Ser Phe Leu Ala Phe Leu Glu Lys	Gln Gly		
	145	150	155	160
Lys Ile Asp Glu Asp	Asn Leu Thr Cys Leu Glu Asp	Leu Cys Lys Thr		
	165	170	175	
Val Val Pro Lys Leu Leu Arg	Asn Ile Glu Lys Tyr Lys Arg	Glu Lys		
	180	185	190	
Ala Ile Gln Ile Val Thr	Pro Pro Val Asp Lys Glu Ala Glu Ser Tyr			
	195	200	205	
Gln Gly Glu Glu Glu Leu Val	Ser Gln Thr Asp Val Lys Thr Phe Leu			
	210	215	220	
Glu Ala Leu Pro Arg Ala Ala Val	Tyr Arg Met Asn Arg Asn His Arg			
	225	230	235	240
Gly Leu Cys Val Ile Val Asn Asn	His Ser Phe Thr Ser Leu Lys Asp			
	245	250	255	
Arg Gln Gly Thr His Lys Asp Ala	Glu Ile Leu Ser His Val Phe Gln			
	260	265	270	
Trp Leu Gly Phe Thr Val His Ile His	Asn Asn Val Thr Lys Val Glu			
	275	280	285	

Met Glu Met Val Leu Gln Lys Gln Lys Cys Asn Pro Ala His Ala Asp
 290 295 300

Gly Asp Cys Phe Val Phe Cys Ile Leu Thr His Gly Arg Phe Gly Ala
 305 310 315 320

Val Tyr Ser Ser Asp Glu Ala Leu Ile Pro Ile Arg Glu Ile Met Ser
 325 330 335

His Phe Thr Ala Leu Gln Cys Pro Arg Leu Ala Glu Lys Pro Lys Leu
 340 345 350

Phe Phe Ile Gln Ala Cys Gln Gly Glu Glu Ile Gln Pro Ser Val Ser
 355 360 365

Ile Glu Ala Asp Ala Leu Asn Pro Glu Gln Ala Pro Thr Ser Leu Gln
 370 375 380

Asp Ser Ile Pro Ala Glu Ala Asp Phe Leu Leu Gly Leu Ala Thr Val
 385 390 395 400

Pro Gly Tyr Val Ser Phe Arg His Val Glu Glu Gly Ser Trp Tyr Ile
 405 410 415

Gln Ser Leu Cys Asn His Leu Lys Lys Leu Val Pro Arg His Glu Asp
 420 425 430

Ile Leu Ser Ile Leu Thr Ala Val Asn Asp Asp Val Ser Arg Arg Val
 435 440 445

Asp Lys Gln Gly Thr Lys Lys Gln Met Pro Gln Pro Ala Phe Thr Leu
 450 455 460

Arg Lys Lys Leu Val Phe Pro Val Pro Leu Asp Ala Leu Ser Ile
 465 470 475

<210> 133
 <211> 509
 <212> PRT
 <213> Human

<400> 133

Met Thr Val Glu Gly Arg Leu Leu Val Pro Asp Arg Ile Asn Gly Thr
 1 5 10 15

Ala Asn Lys Met Asn Gly Ala Leu Asp His Ser Asp Gln Pro Asp Pro
 20 25 30

Asp Ala Ile Lys Met Phe Val Gly Gln Ile Pro Arg Ser Trp Ser Glu
 35 40 45

Lys Glu Leu Lys Glu Leu Phe Glu Pro Tyr Gly Ala Val Tyr Gln Ile
 50 55 60

Asn Val Leu Arg Asp Arg Ser Gln Asn Pro Pro Gln Ser Lys Gly Cys
 65 70 75 80

Cys Phe Val Thr Phe Tyr Thr Arg Lys Ala Ala Leu Glu Ala Gln Asn
 85 90 95

Ala Leu His Asn Ile Lys Thr Leu Pro Gly Met His His Pro Ile Gln
 100 105 110

Met Lys Pro Ala Asp Ser Glu Lys Ser Asn Ala Val Glu Asp Arg Lys
 115 120 125

Leu Phe Ile Gly Met Val Ser Lys Lys Cys Asn Glu Asn Asp Ile Arg
 130 135 140

Val Met Phe Ser Pro Phe Gly Gln Ile Glu Glu Cys Arg Ile Leu Arg
 145 150 155 160

Gly Pro Asp Gly Leu Ser Arg Gly Cys Ala Phe Val Thr Phe Ser Thr
 165 170 175

Arg Ala Met Ala Gln Asn Ala Ile Lys Ala Met His Gln Ser Gln Thr
 180 185 190

Met Glu Gly Cys Ser Ser Pro Ile Val Val Lys Phe Ala Asp Thr Gln
 195 200 205

Lys Asp Lys Glu Gln Arg Arg Leu Gln Gln Gln Leu Ala Gln Gln Met
 210 215 220

Gln Gln Leu Asn Thr Ala Thr Trp Gly Asn Leu Thr Gly Leu Gly Gly
 225 230 235 240

Leu Thr Pro Gln Tyr Leu Ala Leu Leu Gln Gln Ala Thr Ser Ser Ser
 245 250 255

Asn Leu Gly Ala Phe Ser Gly Ile Gln Gln Met Ala Gly Met Asn Ala
 260 265 270

Leu Gln Leu Gln Asn Leu Ala Thr Leu Ala Ala Ala Ala Ala Ala Ala
 275 280 285

Gln Thr Ser Ala Thr Ser Thr Asn Ala Asn Pro Leu Ser Thr Thr Ser
 290 295 300

Ser Ala Leu Gly Ala Leu Thr Ser Pro Val Ala Ala Ser Thr Pro Asn
 305 310 315 320

Ser Thr Ala Gly Ala Ala Met Asn Ser Leu Thr Ser Leu Gly Thr Leu
 325 330 335

Gln Gly Leu Ala Gly Ala Thr Val Gly Leu Asn Asn Ile Asn Ala Leu
 340 345 350

Ala Val Ala Gln Met Leu Ser Gly Met Ala Ala Leu Asn Gly Gly Leu
 355 360 365

Gly Ala Thr Gly Leu Thr Asn Gly Thr Ala Gly Thr Met Asp Ala Leu
 370 375 380

Thr Gln Ala Tyr Ser Gly Ile Gln Gln Tyr Ala Ala Ala Ala Leu Pro
 385 390 395 400

Thr Leu Tyr Ser Gln Ser Leu Leu Gln Gln Gln Ser Ala Ala Gly Ser
 405 410 415

Gln Lys Glu Gly Pro Glu Gly Ala Asn Leu Phe Ile Tyr His Leu Pro
 420 425 430

Gln Glu Phe Gly Asp Gln His Ile Leu Gln Met Phe Met Pro Phe Gly
 435 440 445

Asn Val Ile Ser Ala Lys Val Phe Ile Asp Lys Gln Thr Asn Leu Ser
 450 455 460

Lys Cys Phe Gly Phe Val Ser Tyr Asp Asn Pro Val Ser Ala Gln Ala
 465 470 475 480

Ala Ile Gln Ala Met Asn Gly Phe Gln Ile Gly Met Lys Arg Leu Lys
 485 490 495

Val Gln Leu Lys Arg Ser Lys Asn Asp Ser Lys Pro Tyr
 500 505

<210> 134
 <211> 141
 <212> PRT
 <213> Human

<400> 134

Met Ala Arg Pro Leu Cys Thr Leu Leu Leu Leu Met Ala Thr Leu Ala
 1 5 10 15

Gly Ala Leu Ala Ser Ser Ser Lys Glu Glu Asn Arg Ile Ile Pro Gly
 20 25 30

Gly Ile Tyr Asp Ala Asp Leu Asn Asp Glu Trp Val Gln Arg Ala Leu
 35 40 45

His Phe Ala Ile Ser Glu Tyr Asn Lys Ala Thr Glu Asp Glu Tyr Tyr
 50 55 60

Arg Arg Pro Leu Gln Val Leu Arg Ala Arg Glu Gln Thr Phe Gly Gly
 65 70 75 80

Val Asn Tyr Phe Phe Asp Val Glu Val Gly Arg Thr Ile Cys Thr Lys
 85 90 95

Ser Gln Pro Asn Leu Asp Thr Cys Ala Phe His Glu Gln Pro Glu Leu
 100 105 110

Gln Lys Lys Gln Leu Cys Ser Phe Glu Ile Tyr Glu Val Pro Trp Glu
 115 120 125

Asp Arg Met Ser Leu Val Asn Ser Arg Cys Gln Glu Ala
 130 135 140

<210> 135
 <211> 1480
 <212> PRT
 <213> Human

<400> 135

Met Gln Arg Ser Pro Leu Glu Lys Ala Ser Val Val Ser Lys Leu Phe
 1 5 10 15

Phe Ser Trp Thr Arg Pro Ile Leu Arg Lys Gly Tyr Arg Gln Arg Leu
 20 25 30

Glu Leu Ser Asp Ile Tyr Gln Ile Pro Ser Val Asp Ser Ala Asp Asn
 35 40 45

Leu Ser Glu Lys Leu Glu Arg Glu Trp Asp Arg Glu Leu Ala Ser Lys
 50 55 60

Lys Asn Pro Lys Leu Ile Asn Ala Leu Arg Arg Cys Phe Phe Trp Arg
 65 70 75 80

Phe Met Phe Tyr Gly Ile Phe Leu Tyr Leu Gly Glu Val Thr Lys Ala
 85 90 95

Val Gln Pro Leu Leu Leu Gly Arg Ile Ile Ala Ser Tyr Asp Pro Asp
 100 105 110

Asn Lys Glu Glu Arg Ser Ile Ala Ile Tyr Leu Gly Ile Gly Leu Cys
 115 120 125

Leu Leu Phe Ile Val Arg Thr Leu Leu Leu His Pro Ala Ile Phe Gly
 130 135 140

Leu His His Ile Gly Met Gln Met Arg Ile Ala Met Phe Ser Leu Ile
 145 150 155 160

Tyr Lys Lys Thr Leu Lys Leu Ser Ser Arg Val Leu Asp Lys Ile Ser
 165 170 175

Ile Gly Gln Leu Val Ser Leu Leu Ser Asn Asn Leu Asn Lys Phe Asp
 180 185 190

Glu Gly Leu Ala Leu Ala His Phe Val Trp Ile Ala Pro Leu Gln Val
 195 200 205

Ala Leu Leu Met Gly Leu Ile Trp Glu Leu Leu Gln Ala Ser Ala Phe
 210 215 220

Cys Gly Leu Gly Phe Leu Ile Val Leu Ala Leu Phe Gln Ala Gly Leu
 225 230 235 240

Gly Arg Met Met Met Lys Tyr Arg Asp Gln Arg Ala Gly Lys Ile Ser
 245 250 255

Glu Arg Leu Val Ile Thr Ser Glu Met Ile Glu Asn Ile Gln Ser Val
260 265 270

Lys Ala Tyr Cys Trp Glu Glu Ala Met Glu Lys Met Ile Glu Asn Leu
275 280 285

Arg Gln Thr Glu Leu Lys Leu Thr Arg Lys Ala Ala Tyr Val Arg Tyr
290 295 300

Phe Asn Ser Ser Ala Phe Phe Phe Ser Gly Phe Phe Val Val Phe Leu
305 310 315 320

Ser Val Leu Pro Tyr Ala Leu Ile Lys Gly Ile Ile Leu Arg Lys Ile
325 330 335

Phe Thr Thr Ile Ser Phe Cys Ile Val Leu Arg Met Ala Val Thr Arg
340 345 350

Gln Phe Pro Trp Ala Val Gln Thr Trp Tyr Asp Ser Leu Gly Ala Ile
355 360 365

Asn Lys Ile Gln Asp Phe Leu Gln Lys Gln Glu Tyr Lys Thr Leu Glu
370 375 380

Tyr Asn Leu Thr Thr Thr Glu Val Val Met Glu Asn Val Thr Ala Phe
385 390 395 400

Trp Glu Glu Gly Phe Gly Glu Leu Phe Glu Lys Ala Lys Gln Asn Asn
405 410 415

Asn Asn Arg Lys Thr Ser Asn Gly Asp Asp Ser Leu Phe Phe Ser Asn
420 425 430

Phe Ser Leu Leu Gly Thr Pro Val Leu Lys Asp Ile Asn Phe Lys Ile
435 440 445

Glu Arg Gly Gln Leu Leu Ala Val Ala Gly Ser Thr Gly Ala Gly Lys
450 455 460

Thr Ser Leu Leu Met Met Ile Met Gly Glu Leu Glu Pro Ser Glu Gly
465 470 475 480

Lys Ile Lys His Ser Gly Arg Ile Ser Phe Cys Ser Gln Phe Ser Trp

485	490	495
Ile Met Pro Gly Thr Ile Lys Glu Asn Ile Ile Phe Gly Val Ser Tyr 500 505 510		
Asp Glu Tyr Arg Tyr Arg Ser Val Ile Lys Ala Cys Gln Leu Glu Glu 515 520 525		
Asp Ile Ser Lys Phe Ala Glu Lys Asp Asn Ile Val Leu Gly Glu Gly 530 535 540		
Gly Ile Thr Leu Ser Gly Gly Gln Arg Ala Arg Ile Ser Leu Ala Arg 545 550 555 560		
Ala Val Tyr Lys Asp Ala Asp Leu Tyr Leu Leu Asp Ser Pro Phe Gly 565 570 575		
Tyr Leu Asp Val Leu Thr Glu Lys Glu Ile Phe Glu Ser Cys Val Cys 580 585 590		
Lys Leu Met Ala Asn Lys Thr Arg Ile Leu Val Thr Ser Lys Met Glu 595 600 605		
His Leu Lys Lys Ala Asp Lys Ile Leu Ile Leu Asn Glu Gly Ser Ser 610 615 620		
Tyr Phe Tyr Gly Thr Phe Ser Glu Leu Gln Asn Leu Gln Pro Asp Phe 625 630 635 640		
Ser Ser Lys Leu Met Gly Cys Asp Ser Phe Asp Gln Phe Ser Ala Glu 645 650 655		
Arg Arg Asn Ser Ile Leu Thr Glu Thr Leu His Arg Phe Ser Leu Glu 660 665 670		
Gly Asp Ala Pro Val Ser Trp Thr Glu Thr Lys Lys Gln Ser Phe Lys 675 680 685		
Gln Thr Gly Glu Phe Gly Glu Lys Arg Lys Asn Ser Ile Leu Asn Pro 690 695 700		
Ile Asn Ser Ile Arg Lys Phe Ser Ile Val Gln Lys Thr Pro Leu Gln 705 710 715 720		

Met	Asn	Gly	Ile	Glu	Glu	Asp	Ser	Asp	Glu	Pro	Leu	Glu	Arg	Arg	Leu	725	730	735	
Ser	Leu	Val	Pro	Asp	Ser	Glu	Gln	Gly	Glu	Ala	Ile	Leu	Pro	Arg	Ile	740	745	750	
Ser	Val	Ile	Ser	Thr	Gly	Pro	Thr	Leu	Gln	Ala	Arg	Arg	Arg	Gln	Ser	755	760	765	
Val	Leu	Asn	Leu	Met	Thr	His	Ser	Val	Asn	Gln	Gly	Gln	Asn	Ile	His	770	775	780	
Arg	Lys	Thr	Thr	Ala	Ser	Thr	Arg	Lys	Val	Ser	Leu	Ala	Pro	Gln	Ala	785	790	795	800
Asn	Leu	Thr	Glu	Leu	Asp	Ile	Tyr	Ser	Arg	Arg	Leu	Ser	Gln	Glu	Thr	805	810	815	
Gly	Leu	Glu	Ile	Ser	Glu	Glu	Ile	Asn	Glu	Glu	Asp	Leu	Lys	Glu	Cys	820	825	830	
Leu	Phe	Asp	Asp	Met	Glu	Ser	Ile	Pro	Ala	Val	Thr	Thr	Trp	Asn	Thr	835	840	845	
Tyr	Leu	Arg	Tyr	Ile	Thr	Val	His	Lys	Ser	Leu	Ile	Phe	Val	Leu	Ile	850	855	860	
Trp	Cys	Leu	Val	Ile	Phe	Leu	Ala	Glu	Val	Ala	Ala	Ser	Leu	Val	Val	865	870	875	880
Leu	Trp	Leu	Leu	Gly	Asn	Thr	Pro	Leu	Gln	Asp	Lys	Gly	Asn	Ser	Thr	885	890	895	
His	Ser	Arg	Asn	Asn	Ser	Tyr	Ala	Val	Ile	Ile	Thr	Ser	Thr	Ser	Ser	900	905	910	
Tyr	Tyr	Val	Phe	Tyr	Ile	Tyr	Val	Gly	Val	Ala	Asp	Thr	Leu	Leu	Ala	915	920	925	
Met	Gly	Phe	Phe	Arg	Gly	Leu	Pro	Leu	Val	His	Thr	Leu	Ile	Thr	Val	930	935	940	
Ser	Lys	Ile	Leu	His	His	Lys	Met	Leu	His	Ser	Val	Leu	Gln	Ala	Pro	945	950	955	960

Met Ser Thr Leu Asn Thr Leu Lys Ala Gly Gly Ile Leu Asn Arg Phe
965 970 975

Ser Lys Asp Ile Ala Ile Leu Asp Asp Leu Leu Pro Leu Thr Ile Phe
980 985 990

Asp Phe Ile Gln Leu Leu Leu Ile Val Ile Gly Ala Ile Ala Val Val
995 1000 1005

Ala Val Leu Gln Pro Tyr Ile Phe Val Ala Thr Val Pro Val Ile
1010 1015 1020

Val Ala Phe Ile Met Leu Arg Ala Tyr Phe Leu Gln Thr Ser Gln
1025 1030 1035

Gln Leu Lys Gln Leu Glu Ser Glu Gly Arg Ser Pro Ile Phe Thr
1040 1045 1050

His Leu Val Thr Ser Leu Lys Gly Leu Trp Thr Leu Arg Ala Phe
1055 1060 1065

Gly Arg Gln Pro Tyr Phe Glu Thr Leu Phe His Lys Ala Leu Asn
1070 1075 1080

Leu His Thr Ala Asn Trp Phe Leu Tyr Leu Ser Thr Leu Arg Trp
1085 1090 1095

Phe Gln Met Arg Ile Glu Met Ile Phe Val Ile Phe Phe Ile Ala
1100 1105 1110

Val Thr Phe Ile Ser Ile Leu Thr Thr Gly Glu Gly Glu Gly Arg
1115 1120 1125

Val Gly Ile Ile Leu Thr Leu Ala Met Asn Ile Met Ser Thr Leu
1130 1135 1140

Gln Trp Ala Val Asn Ser Ser Ile Asp Val Asp Ser Leu Met Arg
1145 1150 1155

Ser Val Ser Arg Val Phe Lys Phe Ile Asp Met Pro Thr Glu Gly
1160 1165 1170

Lys Pro Thr Lys Ser Thr Lys Pro Tyr Lys Asn Gly Gln Leu Ser
1175 1180 1185

Lys	Val	Met	Ile	Ile	Glu	Asn	Ser	His	Val	Lys	Lys	Asp	Asp	Ile
1190						1195						1200		
Trp	Pro	Ser	Gly	Gly	Gln	Met	Thr	Val	Lys	Asp	Leu	Thr	Ala	Lys
1205						1210					1215			
Tyr	Thr	Glu	Gly	Gly	Asn	Ala	Ile	Leu	Glu	Asn	Ile	Ser	Phe	Ser
1220						1225					1230			
Ile	Ser	Pro	Gly	Gln	Arg	Val	Gly	Leu	Leu	Gly	Arg	Thr	Gly	Ser
1235						1240					1245			
Gly	Lys	Ser	Thr	Leu	Leu	Ser	Ala	Phe	Leu	Arg	Leu	Leu	Asn	Thr
1250						1255					1260			
Glu	Gly	Glu	Ile	Gln	Ile	Asp	Gly	Val	Ser	Trp	Asp	Ser	Ile	Thr
1265						1270					1275			
Leu	Gln	Gln	Trp	Arg	Lys	Ala	Phe	Gly	Val	Ile	Pro	Gln	Lys	Val
1280						1285					1290			
Phe	Ile	Phe	Ser	Gly	Thr	Phe	Arg	Lys	Asn	Leu	Asp	Pro	Tyr	Glu
1295						1300					1305			
Gln	Trp	Ser	Asp	Gln	Glu	Ile	Trp	Lys	Val	Ala	Asp	Glu	Val	Gly
1310						1315					1320			
Leu	Arg	Ser	Val	Ile	Glu	Gln	Phe	Pro	Gly	Lys	Leu	Asp	Phe	Val
1325						1330					1335			
Leu	Val	Asp	Gly	Gly	Cys	Val	Leu	Ser	His	Gly	His	Lys	Gln	Leu
1340						1345					1350			
Met	Cys	Leu	Ala	Arg	Ser	Val	Leu	Ser	Lys	Ala	Lys	Ile	Leu	Leu
1355						1360					1365			
Leu	Asp	Glu	Pro	Ser	Ala	His	Leu	Asp	Pro	Val	Thr	Tyr	Gln	Ile
1370						1375					1380			
Ile	Arg	Arg	Thr	Leu	Lys	Gln	Ala	Phe	Ala	Asp	Cys	Thr	Val	Ile
1385						1390					1395			
Leu	Cys	Glu	His	Arg	Ile	Glu	Ala	Met	Leu	Glu	Cys	Gln	Gln	Phe

1400 1405 1410
 Leu Val Ile Glu Glu Asn Lys Val Arg Gln Tyr Asp Ser Ile Gln
 1415 1420 1425
 Lys Leu Leu Asn Glu Arg Ser Leu Phe Arg Gln Ala Ile Ser Pro
 1430 1435 1440
 Ser Asp Arg Val Lys Leu Phe Pro His Arg Asn Ser Ser Lys Cys
 1445 1450 1455
 Lys Ser Lys Pro Gln Ile Ala Ala Leu Lys Glu Glu Thr Glu Glu
 1460 1465 1470
 Glu Val Gln Asp Thr Arg Leu
 1475 1480

 <210> 136
 <211> 502
 <212> PRT
 <213> Human

 <400> 136
 Met Leu Ala Ala Met Gly Ser Leu Ala Ala Ala Leu Trp Ala Val Val
 1 5 10 15

 His Pro Arg Thr Leu Leu Leu Gly Thr Val Ala Phe Leu Leu Ala Ala
 20 25 30

 Asp Phe Leu Lys Arg Arg Arg Pro Lys Asn Tyr Pro Pro Gly Pro Trp
 35 40 45

 Arg Leu Pro Phe Leu Gly Asn Phe Phe Leu Val Asp Phe Glu Gln Ser
 50 55 60

 His Leu Glu Val Gln Leu Phe Val Lys Lys Tyr Gly Asn Leu Phe Ser
 65 70 75 80

 Leu Glu Leu Gly Asp Ile Ser Ala Val Leu Ile Thr Gly Leu Pro Leu
 85 90 95

 Ile Lys Glu Ala Leu Ile His Met Asp Gln Asn Phe Gly Asn Arg Pro
 100 105 110

 Val Thr Pro Met Arg Glu His Ile Phe Lys Lys Asn Gly Leu Ile Met

115	120	125
Ser Ser Gly Gln Ala Trp Lys Glu Gln Arg Arg Phe Thr Leu Thr Ala		
130	135	140
Leu Arg Asn Phe Gly Leu Gly Lys Lys Ser Leu Glu Glu Arg Ile Gln		
145	150	155
Glu Glu Ala Gln His Leu Thr Glu Ala Ile Lys Glu Glu Asn Gly Gln		
	165	170
Pro Phe Asp Pro His Phe Lys Ile Asn Asn Ala Val Ser Asn Ile Ile		
	180	185
Cys Ser Ile Thr Phe Gly Glu Arg Phe Glu Tyr Gln Asp Ser Trp Phe		
	195	200
Gln Gln Leu Leu Lys Leu Leu Asp Glu Val Thr Tyr Leu Glu Ala Ser		
	210	215
Lys Thr Cys Gln Leu Tyr Asn Val Phe Pro Trp Ile Met Lys Phe Leu		
225	230	235
Pro Gly Pro His Gln Thr Leu Phe Ser Asn Trp Lys Lys Leu Lys Leu		
	245	250
Phe Val Ser His Met Ile Asp Lys His Arg Lys Asp Trp Asn Pro Ala		
	260	265
Glu Thr Arg Asp Phe Ile Asp Ala Tyr Leu Lys Glu Met Ser Lys His		
	275	280
Thr Gly Asn Pro Thr Ser Ser Phe His Glu Glu Asn Leu Ile Cys Ser		
	290	295
Thr Leu Asp Leu Phe Phe Ala Gly Thr Glu Thr Thr Ser Thr Thr Leu		
305	310	315
Arg Trp Ala Leu Leu Tyr Met Ala Leu Tyr Pro Glu Ile Gln Glu Lys		
	325	330
Val Gln Ala Glu Ile Asp Arg Val Ile Gly Gln Gly Gln Gln Pro Ser		
	340	345
		350

Thr Ala Ala Arg Glu Ser Met Pro Tyr Thr Asn Ala Val Ile His Glu
 355 360 365

Val Gln Arg Met Gly Asn Ile Ile Pro Leu Asn Val Pro Arg Glu Val
 370 375 380

Thr Val Asp Thr Thr Leu Ala Gly Tyr His Leu Pro Lys Gly Thr Met
 385 390 395 400

Ile Leu Thr Asn Leu Thr Ala Leu His Arg Asp Pro Thr Glu Trp Ala
 405 410 415

Thr Pro Asp Thr Phe Asn Pro Asp His Phe Leu Glu Asn Gly Gln Phe
 420 425 430

Lys Lys Arg Glu Ala Phe Met Pro Phe Ser Ile Gly Lys Arg Ala Cys
 435 440 445

Leu Gly Glu Gln Leu Ala Arg Thr Glu Leu Phe Ile Phe Phe Thr Ser
 450 455 460

Leu Met Gln Lys Phe Thr Phe Arg Pro Pro Asn Asn Glu Lys Leu Ser
 465 470 475 480

Leu Lys Phe Arg Met Gly Ile Thr Ile Ser Pro Val Ser His Arg Leu
 485 490 495

Cys Ala Val Pro Gln Val
 500

<210> 137
 <211> 766
 <212> PRT
 <213> Human

<400> 137

Met Lys Thr Pro Trp Arg Val Leu Leu Gly Leu Leu Gly Ala Ala Ala
 1 5 10 15

Leu Val Thr Ile Ile Thr Val Pro Val Val Leu Leu Asn Lys Gly Thr
 20 25 30

Asp Asp Ala Thr Ala Asp Ser Arg Lys Thr Tyr Thr Leu Thr Asp Tyr
 35 40 45

Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr Ser Leu Arg Trp Ile Ser
 50 55 60

Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn Asn Ile Leu Val Phe Asn
 65 70 75 80

Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu Glu Asn Ser Thr Phe Asp
 85 90 95

Glu Phe Gly His Ser Ile Asn Asp Tyr Ser Ile Ser Pro Asp Gly Gln
 100 105 110

Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys Gln Trp Arg His Ser Tyr
 115 120 125

Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn Lys Arg Gln Leu Ile Thr
 130 135 140

Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp Val Thr Trp Ser Pro Val
 145 150 155 160

Gly His Lys Leu Ala Tyr Val Trp Asn Asn Asp Ile Tyr Val Lys Ile
 165 170 175

Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr Trp Thr Gly Lys Glu Asp
 180 185 190

Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val Tyr Glu Glu Glu Val Phe
 195 200 205

Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro Asn Gly Thr Phe Leu Ala
 210 215 220

Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro Leu Ile Glu Tyr Ser Phe
 225 230 235 240

Tyr Ser Asp Glu Ser Leu Gln Tyr Pro Lys Thr Val Arg Val Pro Tyr
 245 250 255

Pro Lys Ala Gly Ala Val Asn Pro Thr Val Lys Phe Phe Val Val Asn
 260 265 270

Thr Asp Ser Leu Ser Ser Val Thr Asn Ala Thr Ser Ile Gln Ile Thr
 275 280 285

Ala Pro Ala Ser Met Leu Ile Gly Asp His Tyr Leu Cys Asp Val Thr
 290 295 300

Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln Trp Leu Arg Arg Ile Gln
 305 310 315 320

Asn Tyr Ser Val Met Asp Ile Cys Asp Tyr Asp Glu Ser Ser Gly Arg
 325 330 335

Trp Asn Cys Leu Val Ala Arg Gln His Ile Glu Met Ser Thr Thr Gly
 340 345 350

Trp Val Gly Arg Phe Arg Pro Ser Glu Pro His Phe Thr Leu Asp Gly
 355 360 365

Asn Ser Phe Tyr Lys Ile Ile Ser Asn Glu Glu Gly Tyr Arg His Ile
 370 375 380

Cys Tyr Phe Gln Ile Asp Lys Lys Asp Cys Thr Phe Ile Thr Lys Gly
 385 390 395 400

Thr Trp Glu Val Ile Gly Ile Glu Ala Leu Thr Ser Asp Tyr Leu Tyr
 405 410 415

Tyr Ile Ser Asn Glu Tyr Lys Gly Met Pro Gly Gly Arg Asn Leu Tyr
 420 425 430

Lys Ile Gln Leu Ser Asp Tyr Thr Lys Val Thr Cys Leu Ser Cys Glu
 435 440 445

Leu Asn Pro Glu Arg Cys Gln Tyr Tyr Ser Val Ser Phe Ser Lys Glu
 450 455 460

Ala Lys Tyr Tyr Gln Leu Arg Cys Ser Gly Pro Gly Leu Pro Leu Tyr
 465 470 475 480

Thr Leu His Ser Ser Val Asn Asp Lys Gly Leu Arg Val Leu Glu Asp
 485 490 495

Asn Ser Ala Leu Asp Lys Met Leu Gln Asn Val Gln Met Pro Ser Lys
 500 505 510

Lys Leu Asp Phe Ile Ile Leu Asn Glu Thr Lys Phe Trp Tyr Gln Met
 515 520 525

Ile Leu Pro Pro His Phe Asp Lys Ser Lys Lys Tyr Pro Leu Leu Leu
 530 535 540

Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys Ala Asp Ile Val Phe Arg
 545 550 555 560

Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr Glu Asn Ile Ile Val Ala
 565 570 575

Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln Gly Asp Lys Ile Met His
 580 585 590

Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu Val Glu Asp Gln Ile Glu
 595 600 605

Ala Ala Arg Gln Phe Ser Lys Met Gly Phe Val Asp Asn Lys Arg Ile
 610 615 620

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Thr Ser Met Val Leu
 625 630 635 640

Gly Ser Gly Ser Gly Val Phe Lys Cys Gly Ile Ala Val Ala Pro Val
 645 650 655

Ser Arg Trp Glu Tyr Tyr Glu Ser Val Tyr Thr Glu Arg Tyr Met Gly
 660 665 670

Leu Pro Thr Pro Glu Asp Asn Leu Asp His Tyr Arg Asn Ser Thr Val
 675 680 685

Met Ser Arg Ala Glu Asn Phe Lys Gln Val Glu Tyr Leu Leu Ile His
 690 695 700

Gly Thr Ala Asp Asp Asn Val His Phe Gln Gln Ser Ala Gln Ile Ser
 705 710 715 720

Lys Ala Leu Val Asp Val Gly Val Asp Phe Gln Ala Met Trp Tyr Thr
 725 730 735

Asp Glu Asp His Gly Ile Ala Ser Ser Thr Ala His Gln His Ile Tyr
 740 745 750

Thr His Met Ser His Phe Ile Lys Gln Cys Phe Ser Leu Pro

755

760

765

<210> 138
 <211> 984
 <212> PRT
 <213> Human

<400> 138

Met Glu Arg Arg Trp Pro Leu Gly Leu Gly Leu Val Leu Leu Leu Cys
 1 5 10 15

Ala Pro Leu Pro Pro Gly Ala Arg Ala Lys Glu Val Thr Leu Met Asp
 20 25 30

Thr Ser Lys Ala Gln Gly Glu Leu Gly Trp Leu Leu Asp Pro Pro Lys
 35 40 45

Asp Gly Trp Ser Glu Gln Gln Gln Ile Leu Asn Gly Thr Pro Leu Tyr
 50 55 60

Met Tyr Gln Asp Cys Pro Met Gln Gly Arg Arg Asp Thr Asp His Trp
 65 70 75 80

Leu Arg Ser Asn Trp Ile Tyr Arg Gly Glu Glu Ala Ser Arg Val His
 85 90 95

Val Glu Leu Gln Phe Thr Val Arg Asp Cys Lys Ser Phe Pro Gly Gly
 100 105 110

Ala Gly Pro Leu Gly Cys Lys Glu Thr Phe Asn Leu Leu Tyr Met Glu
 115 120 125

Ser Asp Gln Asp Val Gly Ile Gln Leu Arg Arg Pro Leu Phe Gln Lys
 130 135 140

Val Thr Thr Val Ala Ala Asp Gln Ser Phe Thr Ile Arg Asp Leu Ala
 145 150 155 160

Ser Gly Ser Val Lys Leu Asn Val Glu Arg Cys Ser Leu Gly Arg Leu
 165 170 175

Thr Arg Arg Gly Leu Tyr Leu Ala Phe His Asn Pro Gly Ala Cys Val
 180 185 190

Ala Leu Val Ser Val Arg Val Phe Tyr Gln Arg Cys Pro Glu Thr Leu

195 200 205
 Asn Gly Leu Ala Gln Phe Pro Asp Thr Leu Pro Gly Pro Ala Gly Leu
 210 215 220
 Val Glu Val Ala Gly Thr Cys Leu Pro His Ala Arg Ala Ser Pro Arg
 225 230 235 240
 Pro Ser Gly Ala Pro Arg Met His Cys Ser Pro Asp Gly Glu Trp Leu
 245 250 255
 Val Pro Val Gly Arg Cys His Cys Glu Pro Gly Tyr Glu Glu Gly Gly
 260 265 270
 Ser Gly Glu Ala Cys Val Ala Cys Pro Ser Gly Ser Tyr Arg Met Asp
 275 280 285
 Met Asp Thr Pro His Cys Leu Thr Cys Pro Gln Gln Ser Thr Ala Glu
 290 295 300
 Ser Glu Gly Ala Thr Ile Cys Thr Cys Glu Ser Gly His Tyr Arg Ala
 305 310 315 320
 Pro Gly Glu Gly Pro Gln Val Ala Cys Thr Gly Pro Pro Ser Ala Pro
 325 330 335
 Arg Asn Leu Ser Phe Ser Ala Ser Gly Thr Gln Leu Ser Leu Arg Trp
 340 345 350
 Glu Pro Pro Ala Asp Thr Gly Gly Arg Gln Asp Val Arg Tyr Ser Val
 355 360 365
 Arg Cys Ser Gln Cys Gln Gly Thr Ala Gln Asp Gly Gly Pro Cys Gln
 370 375 380
 Pro Cys Gly Val Gly Val His Phe Ser Pro Gly Ala Arg Ala Leu Thr
 385 390 395 400
 Thr Pro Ala Val His Val Asn Gly Leu Glu Pro Tyr Ala Asn Tyr Thr
 405 410 415
 Phe Asn Val Glu Ala Gln Asn Gly Val Ser Gly Leu Gly Ser Ser Gly
 420 425 430

His Ala Ser Thr Ser Val Ser Ile Ser Met Gly His Ala Glu Ser Leu
 435 440 445

Ser Gly Leu Ser Leu Arg Leu Val Lys Lys Glu Pro Arg Gln Leu Glu
 450 455 460

Leu Thr Trp Ala Gly Ser Arg Pro Arg Ser Pro Gly Ala Asn Leu Thr
 465 470 475 480

Tyr Glu Leu His Val Leu Asn Gln Asp Glu Glu Arg Tyr Gln Met Val
 485 490 495

Leu Glu Pro Arg Val Leu Leu Thr Glu Leu Gln Pro Asp Thr Thr Tyr
 500 505 510

Ile Val Arg Val Arg Met Leu Thr Pro Leu Gly Pro Gly Pro Phe Ser
 515 520 525

Pro Asp His Glu Phe Arg Thr Ser Pro Pro Val Ser Arg Gly Leu Thr
 530 535 540

Gly Gly Glu Ile Val Ala Val Ile Phe Gly Leu Leu Leu Gly Ala Ala
 545 550 555 560

Leu Leu Leu Gly Ile Leu Val Phe Arg Ser Arg Arg Ala Gln Arg Gln
 565 570 575

Arg Gln Gln Arg His Val Thr Ala Pro Pro Met Trp Ile Glu Arg Thr
 580 585 590

Ser Cys Ala Glu Ala Leu Cys Gly Thr Ser Arg His Thr Arg Thr Leu
 595 600 605

His Arg Glu Pro Trp Thr Leu Pro Gly Gly Trp Ser Asn Phe Pro Ser
 610 615 620

Arg Glu Leu Asp Pro Ala Trp Leu Met Val Asp Thr Val Ile Gly Glu
 625 630 635 640

Gly Glu Phe Gly Glu Val Tyr Arg Gly Thr Leu Arg Leu Pro Ser Gln
 645 650 655

Asp Cys Lys Thr Val Ala Ile Lys Thr Leu Lys Asp Thr Ser Pro Gly
 660 665 670

Gly Gln Trp Trp Asn Phe Leu Arg Glu Ala Thr Ile Met Gly Gln Phe
 675 680 685

Ser His Pro His Ile Leu His Leu Glu Gly Val Val Thr Lys Arg Lys
 690 695 700

Pro Ile Met Ile Ile Thr Glu Phe Met Glu Asn Ala Ala Leu Asp Ala
 705 710 715 720

Phe Leu Arg Glu Arg Glu Asp Gln Leu Val Pro Gly Gln Leu Val Ala
 725 730 735

Met Leu Gln Gly Ile Ala Ser Gly Met Asn Tyr Leu Ser Asn His Asn
 740 745 750

Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Gln Asn
 755 760 765

Leu Cys Cys Lys Val Ser Asp Phe Gly Leu Thr Arg Leu Leu Asp Asp
 770 775 780

Phe Asp Gly Thr Tyr Glu Thr Gln Gly Gly Lys Ile Pro Ile Arg Trp
 785 790 795 800

Thr Ala Pro Glu Ala Ile Ala His Arg Ile Phe Thr Thr Ala Ser Asp
 805 810 815

Val Trp Ser Phe Gly Ile Val Met Trp Glu Val Leu Ser Phe Gly Asp
 820 825 830

Lys Pro Tyr Gly Glu Met Ser Asn Gln Glu Val Met Lys Ser Ile Glu
 835 840 845

Asp Gly Tyr Arg Leu Pro Pro Pro Val Asp Cys Pro Ala Pro Leu Tyr
 850 855 860

Glu Leu Met Lys Asn Cys Trp Ala Tyr Asp Arg Ala Arg Arg Pro His
 865 870 875 880

Phe Gln Lys Leu Gln Ala His Leu Glu Gln Leu Leu Ala Asn Pro His
 885 890 895

Ser Leu Arg Thr Ile Ala Asn Phe Asp Pro Arg Val Thr Leu Arg Leu
 900 905 910

Pro Ser Leu Ser Gly Ser Asp Gly Ile Pro Tyr Arg Thr Val Ser Glu
 915 920 925

Trp Leu Glu Ser Ile Arg Met Lys Arg Tyr Ile Leu His Phe His Ser
 930 935 940

Ala Gly Leu Asp Thr Met Glu Cys Val Leu Glu Leu Thr Ala Glu Asp
 945 950 955 960

Leu Thr Gln Met Gly Ile Thr Leu Pro Gly His Gln Lys Arg Ile Leu
 965 970 975

Cys Ser Ile Gln Gly Phe Lys Asp
 980

<210> 139
 <211> 822
 <212> PRT
 <213> Human

<400> 139

Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
 1 5 10 15

Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
 20 25 30

Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
 35 40 45

Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
 50 55 60

Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
 65 70 75 80

Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
 85 90 95

Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
 100 105 110

Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
 115 120 125

Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
 130 135 140

Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
 145 150 155 160

Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
 165 170 175

Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
 180 185 190

Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
 195 200 205

Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
 210 215 220

Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
 225 230 235 240

Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
 245 250 255

Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
 260 265 270

Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
 275 280 285

Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
 290 295 300

Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser
 305 310 315 320

Asn Ala Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly
 325 330 335

Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser
 340 345 350

Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys

355	360	365
Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile 370 375 380		
Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg 385 390 395 400		
Met Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val 405 410 415		
His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser 420 425 430		
Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile 435 440 445		
Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val 450 455 460		
Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp 465 470 475 480		
Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val 485 490 495		
Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala 500 505 510		
Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp 515 520 525		
Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys 530 535 540		
His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro 545 550 555 560		
Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr 565 570 575		
Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn 580 585 590		

Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr
595 600 605

Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile
610 615 620

His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val
625 630 635 640

Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp
645 650 655

Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
660 665 670

Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp
675 680 685

Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro
690 695 700

Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly
705 710 715 720

His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met
725 730 735

Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys
740 745 750

Gln Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu
755 760 765

Glu Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr
770 775 780

Pro Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser
785 790 795 800

Pro Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile
805 810 815

Asn Gly Ser Val Lys Thr
820

<210> 140
 <211> 87
 <212> PRT
 <213> Human

<400> 140

Met Gln Lys Val Thr Leu Gly Leu Leu Val Phe Leu Ala Gly Phe Pro
 1 5 10 15

Val Leu Asp Ala Asn Asp Leu Glu Asp Lys Asn Ser Pro Phe Tyr Tyr
 20 25 30

Asp Trp His Ser Leu Gln Val Gly Gly Leu Ile Cys Ala Gly Val Leu
 35 40 45

Cys Ala Met Gly Ile Ile Ile Val Met Ser Ala Lys Cys Lys Cys Lys
 50 55 60

Phe Gly Gln Lys Ser Gly His His Pro Gly Glu Thr Pro Pro Leu Ile
 65 70 75 80

Thr Pro Gly Ser Ala Gln Ser
 85

<210> 141
 <211> 907
 <212> PRT
 <213> Human

<400> 141

Met Asp Thr Ser Arg Leu Gly Val Leu Leu Ser Leu Pro Val Leu Leu
 1 5 10 15

Gln Leu Ala Thr Gly Gly Ser Ser Pro Arg Ser Gly Val Leu Leu Arg
 20 25 30

Gly Cys Pro Thr His Cys His Cys Glu Pro Asp Gly Arg Met Leu Leu
 35 40 45

Arg Val Asp Cys Ser Asp Leu Gly Leu Ser Glu Leu Pro Ser Asn Leu
 50 55 60

Ser Val Phe Thr Ser Tyr Leu Asp Leu Ser Met Asn Asn Ile Ser Gln
 65 70 75 80

Leu Leu Pro Asn Pro Leu Pro Ser Leu Arg Phe Leu Glu Glu Leu Arg
 85 90 95

Leu Ala Gly Asn Ala Leu Thr Tyr Ile Pro Lys Gly Ala Phe Thr Gly
 100 105 110

Leu Tyr Ser Leu Lys Val Leu Met Leu Gln Asn Asn Gln Leu Arg His
 115 120 125

Val Pro Thr Glu Ala Leu Gln Asn Leu Arg Ser Leu Gln Ser Leu Arg
 130 135 140

Leu Asp Ala Asn His Ile Ser Tyr Val Pro Pro Ser Cys Phe Ser Gly
 145 150 155 160

Leu His Ser Leu Arg His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu
 165 170 175

Ile Pro Val Gln Ala Phe Arg Ser Leu Ser Ala Leu Gln Ala Met Thr
 180 185 190

Leu Ala Leu Asn Lys Ile His His Ile Pro Asp Tyr Ala Phe Gly Asn
 195 200 205

Leu Ser Ser Leu Val Val Leu His Leu His Asn Asn Arg Ile His Ser
 210 215 220

Leu Gly Lys Lys Cys Phe Asp Gly Leu His Ser Leu Glu Thr Leu Asp
 225 230 235 240

Leu Asn Tyr Asn Asn Leu Asp Glu Phe Pro Thr Ala Ile Arg Thr Leu
 245 250 255

Ser Asn Leu Lys Glu Leu Gly Phe His Ser Asn Asn Ile Arg Ser Ile
 260 265 270

Pro Glu Lys Ala Phe Val Gly Asn Pro Ser Leu Ile Thr Ile His Phe
 275 280 285

Tyr Asp Asn Pro Ile Gln Phe Val Gly Arg Ser Ala Phe Gln His Leu
 290 295 300

Pro Glu Leu Arg Thr Leu Thr Leu Asn Gly Ala Ser Gln Ile Thr Glu
 305 310 315 320

Phe Pro Asp Leu Thr Gly Thr Ala Asn Leu Glu Ser Leu Thr Leu Thr
 325 330 335

Gly Ala Gln Ile Ser Ser Leu Pro Gln Thr Val Cys Asn Gln Leu Pro
 340 345 350

Asn Leu Gln Val Leu Asp Leu Ser Tyr Asn Leu Leu Glu Asp Leu Pro
 355 360 365

Ser Phe Ser Val Cys Gln Lys Leu Gln Lys Ile Asp Leu Arg His Asn
 370 375 380

Glu Ile Tyr Glu Ile Lys Val Asp Thr Phe Gln Gln Leu Leu Ser Leu
 385 390 395 400

Arg Ser Leu Asn Leu Ala Trp Asn Lys Ile Ala Ile Ile His Pro Asn
 405 410 415

Ala Phe Ser Thr Leu Pro Ser Leu Ile Lys Leu Asp Leu Ser Ser Asn
 420 425 430

Leu Leu Ser Ser Phe Pro Ile Thr Gly Leu His Gly Leu Thr His Leu
 435 440 445

Lys Leu Thr Gly Asn His Ala Leu Gln Ser Leu Ile Ser Ser Glu Asn
 450 455 460

Phe Pro Glu Leu Lys Val Ile Glu Met Pro Tyr Ala Tyr Gln Cys Cys
 465 470 475 480

Ala Phe Gly Val Cys Glu Asn Ala Tyr Lys Ile Ser Asn Gln Trp Asn
 485 490 495

Lys Gly Asp Asn Ser Ser Met Asp Asp Leu His Lys Lys Asp Ala Gly
 500 505 510

Met Phe Gln Ala Gln Asp Glu Arg Asp Leu Glu Asp Phe Leu Leu Asp
 515 520 525

Phe Glu Glu Asp Leu Lys Ala Leu His Ser Val Gln Cys Ser Pro Ser
 530 535 540

Pro Gly Pro Phe Lys Pro Cys Glu His Leu Leu Asp Gly Trp Leu Ile
 545 550 555 560

Arg Ile Gly Val Trp Thr Ile Ala Val Leu Ala Leu Thr Cys Asn Ala
565 570 575

Leu Val Thr Ser Thr Val Phe Arg Ser Pro Leu Tyr Ile Ser Pro Ile
580 585 590

Lys Leu Leu Ile Gly Val Ile Ala Ala Val Asn Met Leu Thr Gly Val
595 600 605

Ser Ser Ala Val Leu Ala Gly Val Asp Ala Phe Thr Phe Gly Ser Phe
610 615 620

Ala Arg His Gly Ala Trp Trp Glu Asn Gly Val Gly Cys His Val Ile
625 630 635 640

Gly Phe Leu Ser Ile Phe Ala Ser Glu Ser Ser Val Phe Leu Leu Thr
645 650 655

Leu Ala Ala Leu Glu Arg Gly Phe Ser Val Lys Tyr Ser Ala Lys Phe
660 665 670

Glu Thr Lys Ala Pro Phe Ser Ser Leu Lys Val Ile Ile Leu Leu Cys
675 680 685

Ala Leu Leu Ala Leu Thr Met Ala Ala Val Pro Leu Leu Gly Gly Ser
690 695 700

Lys Tyr Gly Ala Ser Pro Leu Cys Leu Pro Leu Pro Phe Gly Glu Pro
705 710 715 720

Ser Thr Met Gly Tyr Met Val Ala Leu Ile Leu Leu Asn Ser Leu Cys
725 730 735

Phe Leu Met Met Thr Ile Ala Tyr Thr Lys Leu Tyr Cys Asn Leu Asp
740 745 750

Lys Gly Asp Leu Glu Asn Ile Trp Asp Cys Ser Met Val Lys His Ile
755 760 765

Ala Leu Leu Leu Phe Thr Asn Cys Ile Leu Asn Cys Pro Val Ala Phe
770 775 780

Leu Ser Phe Ser Ser Leu Ile Asn Leu Thr Phe Ile Ser Pro Glu Val

Pro Gln Asn Gly Glu Arg Lys Val Asn Trp Leu Gly Ser Lys Glu Gly

330/439

Val Thr Gln Arg Gly Cys Cys Ser Ser Tyr Pro Pro Thr Lys Gly Gly
 325 330 335

Gly Leu Gly Pro Cys Gly Lys Cys Gln Glu Gly Leu Glu Gly Gly Ala
 340 345 350

Ser Gly Ala Ser Glu Pro Ser Glu Glu Val Asn Lys Ala Ser Gly Pro
 355 360 365

Arg Ala Cys Pro Pro Ser His His Thr Lys Leu Lys Lys Thr Trp Leu
 370 375 380

Thr Arg His Ser Glu Gln Phe Glu Cys Pro Arg Gly Cys Pro Glu Val
 385 390 395 400

Glu Glu Arg Pro Val Ala Arg Leu Arg Ala Leu Lys Arg Ala Gly Ser
 405 410 415

Pro Glu Val Gln Gly Ala Met Gly Ser Pro Ala Pro Lys Arg Pro Pro
 420 425 430

Asp Pro Phe Pro Gly Thr Ala Glu Gln Gly Ala Gly Gly Trp Gln Glu
 435 440 445

Val Arg Asp Thr Ser Ile Gly Asn Lys Asp Val Asp Ser Gly Gln His
 450 455 460

Asp Glu Gln Lys Gly Pro Gln Asp Gly Gln Ala Ser Leu Gln Asp Pro
 465 470 475 480

Gly Leu Gln Asp Ile Pro Cys Leu Ala Leu Pro Ala Lys Leu Ala Gln
 485 490 495

Cys Gln Ser Cys Ala Gln Ala Ala Gly Glu Gly Gly Gly His Ala Cys
 500 505 510

His Ser Gln Gln Val Arg Arg Ser Pro Leu Gly Gly Glu Leu Gln Gln
 515 520 525

Glu Glu Asp Thr Ala Thr Asn Ser Ser Ser Glu Glu Gly Pro Gly Ser
 530 535 540

Gly Pro Asp Ser Arg Leu Ser Thr Gly Leu Ala Lys His Leu Leu Ser
 545 550 555 560

Gly Leu Gly Asp Arg Leu Cys Arg Leu Leu Arg Arg Glu Arg Glu Ala
 565 570 575
 Leu Ala Trp Ala Gln Arg Glu Gly Gln Gly Pro Ala Val Thr Glu Asp
 580 585 590
 Ser Pro Gly Ile Pro Arg Cys Cys Ser Arg Cys His His Gly Leu Phe
 595 600 605
 Asn Thr His Trp Arg Cys Pro Arg Cys Ser His Arg Leu Cys Val Ala
 610 615 620
 Cys Gly Arg Val Ala Gly Thr Gly Arg Ala Arg Glu Lys Ala Gly Phe
 625 630 635 640
 Gln Glu Gln Ser Ala Glu Glu Cys Thr Gln Glu Ala Gly His Ala Ala
 645 650 655
 Cys Ser Leu Met Leu Thr Gln Phe Val Ser Ser Gln Ala Leu Ala Glu
 660 665 670
 Leu Ser Thr Ala Met His Gln Val Trp Val Lys Phe Asp Ile Arg Gly
 675 680 685
 His Cys Pro Cys Gln Ala Asp Ala Arg Val Trp Ala Pro Gly Asp Ala
 690 695 700
 Gly Gln Gln Lys Glu Ser Thr Gln Lys Thr Pro Pro Thr Pro Gln Pro
 705 710 715 720
 Ser Cys Asn Gly Asp Thr His Arg Thr Lys Ser Ile Lys Glu Glu Thr
 725 730 735
 Pro Asp Ser Ala Glu Thr Pro Ala Glu Asp Arg Ala Gly Arg Gly Pro
 740 745 750
 Leu Pro Cys Pro Ser Leu Cys Glu Leu Leu Ala Ser Thr Ala Val Lys
 755 760 765
 Leu Cys Leu Gly His Glu Arg Ile His Met Ala Phe Ala Pro Val Thr
 770 775 780
 Pro Ala Leu Pro Ser Asp Asp Arg Ile Thr Asn Ile Leu Asp Ser Ile
 785 790 795 800

Ile Ala Gln Val Val Glu Arg Lys Ile Gln Glu Lys Ala Leu Gly Pro
 805 810 815

Gly Leu Arg Ala Gly Pro Gly Leu Arg Lys Gly Leu Gly Leu Pro Leu
 820 825 830

Ser Pro Val Arg Pro Arg Leu Pro Pro Pro Gly Ala Leu Leu Trp Leu
 835 840 845

Gln Glu Pro Gln Pro Cys Pro Arg Arg Gly Phe His Leu Phe Gln Glu
 850 855 860

His Trp Arg Gln Gly Gln Pro Val Leu Val Ser Gly Ile Gln Arg Thr
 865 870 875 880

Leu Gln Gly Asn Leu Trp Gly Thr Glu Ala Leu Gly Ala Leu Gly Gly
 885 890 895

Gln Val Gln Ala Leu Ser Pro Leu Gly Pro Pro Gln Pro Ser Ser Leu
 900 905 910

Gly Ser Thr Thr Phe Trp Glu Gly Phe Ser Trp Pro Glu Leu Arg Pro
 915 920 925

Lys Ser Asp Glu Gly Ser Val Leu Leu Leu His Arg Ala Leu Gly Asp
 930 935 940

Glu Asp Thr Ser Arg Val Glu Asn Leu Ala Ala Ser Leu Pro Leu Pro
 945 950 955 960

Glu Tyr Cys Ala Leu His Gly Lys Leu Asn Leu Ala Ser Tyr Leu Pro
 965 970 975

Pro Gly Leu Ala Leu Arg Pro Leu Glu Pro Gln Leu Trp Ala Ala Tyr
 980 985 990

Gly Val Ser Pro His Arg Gly His Leu Gly Thr Lys Asn Leu Cys Val
 995 1000 1005

Glu Val Ala Asp Leu Val Ser Ile Leu Val His Ala Asp Thr Pro
 1010 1015 1020

Leu Pro Ala Trp His Arg Ala Gln Lys Asp Phe Leu Ser Gly Leu

1025

1030

1035

Asp Gly Glu Gly Leu Trp Ser Pro Gly Ser Gln Val Ser Thr Val
 1040 1045 1050

Trp His Val Phe Arg Ala Gln Asp Ala Gln Arg Ile Arg Arg Phe
 1055 1060 1065

Leu Gln Met Val Gln Gly Leu Val Ser Thr Val Ser Val Thr Gln
 1070 1075 1080

His Phe Leu Ser Pro Glu Thr Ser Ala Leu Ser Ala Gln Leu Cys
 1085 1090 1095

His Gln Gly Pro Ser Leu Pro Pro Asp Cys His Leu Leu Tyr Ala
 1100 1105 1110

Gln Met Asp Trp Ala Val Phe Gln Ala Val Lys Val Ala Val Gly
 1115 1120 1125

Thr Leu Gln Glu Ala Lys
 1130

<210> 143
 <211> 142
 <212> PRT
 <213> Human

<400> 143

Met Val Leu Ser Pro Ala Asp Lys Thr Asn Val Lys Ala Ala Trp Gly
 1 5 10 15

Lys Val Gly Ala His Ala Gly Glu Tyr Gly Ala Glu Ala Leu Glu Arg
 20 25 30

Met Phe Leu Ser Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asp
 35 40 45

Leu Ser His Gly Ser Ala Gln Val Lys Gly His Gly Lys Lys Val Ala
 50 55 60

Asp Ala Leu Thr Asn Ala Val Ala His Val Asp Asp Met Pro Asn Ala
 65 70 75 80

Leu Ser Ala Leu Ser Asp Leu His Ala His Lys Leu Arg Val Asp Pro

85

90

95

Val Asn Phe Lys Leu Leu Ser His Cys Leu Leu Val Thr Leu Ala Ala
 100 105 110

His Leu Pro Ala Glu Phe Thr Pro Ala Val His Ala Ser Leu Asp Lys
 115 120 125

Phe Leu Ala Ser Val Ser Thr Val Leu Thr Ser Lys Tyr Arg
 130 135 140

<210> 144
 <211> 543
 <212> PRT
 <213> Human

<400> 144

Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
 1 5 10 15

Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
 20 25 30

Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
 35 40 45

Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
 50 55 60

Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
 65 70 75 80

Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
 85 90 95

Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
 100 105 110

Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
 115 120 125

Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
 130 135 140

Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe

145		150		155		160
Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe	165		170		175	
Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu	180		185		190	
Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu	195		200		205	
Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn	210		215		220	
Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser	225		230		235	240
Gln Leu Gly Glu Asp Phe Ile Gln Leu His Lys Leu Leu Arg Lys Ser	245		250		255	
Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg	260		265		270	
Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu	275		280		285	
Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr	290		295		300	
Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile	305		310		315	320
Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly	325		330		335	
Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala	340		345		350	
Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys	355		360		365	
Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val	370		375		380	

Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
 385 390 395 400

Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
 405 410 415

Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
 420 425 430

Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
 435 440 445

Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
 450 455 460

Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
 465 470 475 480

Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
 485 490 495

Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
 500 505 510

Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
 515 520' 525

Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
 530 535 540

<210> 145
 <211> 203
 <212> PRT
 <213> Human

<400> 145

Cys Ser Val Pro Phe Leu Pro Leu Ala Val Pro Val Arg Ala Val His
 1 5 10 15

Arg Leu Leu Glu His Arg His His Ser Val Thr Trp Pro Ala Thr Glu
 20 25 30

Leu Pro Ile Thr Gln Leu Thr Ser Ser Ile Val Arg Arg Val Asn Glu
 35 40 45

Ala Ser Gly Leu Tyr Gln Met Phe Gly Val Leu Ala Asp Val Ile Leu
50 55 60

Leu Lys Glu Thr Gly Gly Glu Val Pro Pro Cys Thr Leu Ala Pro Ala
65 70 75 80

Ser Ala His Gly His Pro Ser His Arg Gly Arg Leu Leu Asn Arg Leu
85 90 95

Asp Cys Pro Asp Arg Ala His Pro Thr Ser Glu Ala Leu Pro Gly Glu
100 105 110

Leu Phe Gly His Arg Phe Ala Lys Leu Leu Cys Arg Val Leu Leu Pro
115 120 125

Val Arg Pro His Ala Pro Glu Val Ala Thr Leu Leu Pro Ala Gly Val
130 135 140

Pro Glu Asp Ala Gly Thr Arg Glu Tyr Arg Glu Pro Leu Ala Ala Gln
145 150 155 160

Ser Gly Glu Gln Ala Pro Ala Gly Leu Cys Pro His Arg Gln Ala Pro
165 170 175

Gly Gly Gln Gln Pro Ala Ala Trp Arg Pro Arg Ala Thr Arg Phe Pro
180 185 190

Pro Gly Ser Arg Ala Ser Gly Ser Val Arg Arg
195 200

<210> 146
<211> 414
<212> PRT
<213> Human

<400> 146

Met Lys Ala Gln Thr Ala Leu Ser Phe Phe Leu Ile Leu Ile Thr Ser
1 5 10 15

Leu Ser Gly Ser Gln Gly Ile Phe Pro Leu Ala Phe Phe Ile Tyr Val
20 25 30

Pro Met Asn Glu Gln Ile Val Ile Gly Arg Leu Asp Glu Asp Ile Ile
35 40 45

Leu Pro Ser Ser Phe Glu Arg Gly Ser Glu Val Val Ile His Trp Lys
 50 55 60
 Tyr Gln Asp Ser Tyr Lys Val His Ser Tyr Tyr Lys Gly Ser Asp His
 65 70 75 80
 Leu Glu Ser Gln Asp Pro Arg Tyr Ala Asn Arg Thr Ser Leu Phe Tyr
 85 90 95
 Asn Glu Ile Gln Asn Gly Asn Ala Ser Leu Phe Phe Arg Arg Val Ser
 100 105 110
 Leu Leu Asp Glu Gly Ile Tyr Thr Cys Tyr Val Gly Thr Ala Ile Gln
 115 120 125
 Val Ile Thr Asn Lys Val Val Leu Lys Val Gly Val Phe Leu Thr Pro
 130 135 140
 Val Met Lys Tyr Glu Lys Arg Asn Thr Asn Ser Phe Leu Ile Cys Ser
 145 150 155 160
 Val Leu Ser Val Tyr Pro Arg Pro Ile Ile Thr Trp Lys Met Asp Asn
 165 170 175
 Thr Pro Ile Ser Glu Asn Asn Met Glu Glu Thr Gly Ser Leu Asp Ser
 180 185 190
 Phe Ser Ile Asn Ser Pro Leu Asn Ile Thr Gly Ser Asn Ser Ser Tyr
 195 200 205
 Glu Cys Thr Ile Glu Asn Ser Leu Leu Lys Gln Thr Trp Thr Gly Arg
 210 215 220
 Trp Thr Met Lys Asp Gly Leu His Lys Met Gln Ser Glu His Val Ser
 225 230 235 240
 Leu Ser Cys Gln Pro Val Asn Asp Tyr Phe Ser Pro Asn Gln Asp Phe
 245 250 255
 Lys Val Thr Trp Ser Arg Met Lys Ser Gly Thr Phe Ser Val Leu Ala
 260 265 270
 Tyr Tyr Leu Ser Ser Ser Gln Asn Thr Ile Ile Asn Glu Ser Arg Phe
 275 280 285

Ser Trp Asn Lys Glu Leu Ile Asn Gln Ser Asp Phe Ser Met Asn Leu
290 295 300

Met Asp Leu Asn Leu Ser Asp Ser Gly Glu Tyr Leu Cys Asn Ile Ser
305 310 315 320

Ser Asp Glu Tyr Thr Leu Leu Thr Ile His Thr Val His Val Glu Pro
325 330 335

Ser Gln Glu Thr Ala Ser His Asn Lys Gly Leu Trp Ile Leu Val Pro
340 345 350

Ser Ala Ile Leu Ala Ala Phe Leu Leu Ile Trp Ser Val Lys Cys Cys
355 360 365

Arg Ala Gln Leu Glu Ala Arg Arg Ser Arg His Pro Ala Asp Gly Ala
370 375 380

Gln Gln Glu Arg Cys Cys Val Pro Pro Gly Glu Arg Cys Pro Ser Ala
385 390 395 400

Pro Asp Asn Gly Glu Glu Asn Val Pro Leu Ser Gly Lys Val
405 410

<210> 147
<211> 545
<212> PRT
<213> Human

<400> 147

Met Val Asp Ala Ala Glu Asn Leu Cys Pro Asn Val Met Lys Lys Ala
1 5 10 15

His Ile Arg Gln Asp Leu Ile His Ala Ser Thr Glu Lys Ile Ser Ile
20 25 30

Pro Arg Thr Phe Val Lys Asn Val Leu Leu Glu Gln Ser Gly Ile Asp
35 40 45

Ile Leu Asn Lys Ile Ser Glu Val Lys Leu Thr Val Ala Ser Phe Leu
50 55 60

Ser Asp Arg Ile Val Asp Glu Ile Leu Asp Ala Leu Ser His Cys His
65 70 75 80

His Lys Leu Ala Asp His Phe Ser Arg Arg Gly Lys Thr Leu Pro Gln
 85 90 95

Gln Glu Ser Leu Glu Ile Glu Leu Ala Glu Glu Arg Pro Val Lys Arg
 100 105 110

Ser Ile Ile Thr Val Glu Glu Leu Thr Glu Ile Glu Arg Leu Glu Asp
 115 120 125

Leu Asp Thr Cys Met Met Thr Pro Lys Ser Lys Arg Lys Ser Ile His
 130 135 140

Ser Arg Met Leu Arg Pro Val Ser Arg Ala Phe Glu Met Glu Phe Asp
 145 150 155 160

Leu Asp Lys Ala Leu Glu Glu Val Pro Ile His Ile Glu Asp Pro Pro
 165 170 175

Phe Pro Ser Leu Arg Gln Glu Lys Arg Ser Ser Gly Phe Ile Ser Glu
 180 185 190

Leu Pro Ser Glu Glu Gly Lys Lys Leu Glu His Phe Thr Lys Leu Arg
 195 200 205

Pro Lys Arg Asn Lys Lys Gln Gln Pro Thr Gln Ala Ala Val Cys Ala
 210 215 220

Ala Asn Ile Val Ser Gln Asp Gly Glu Gln Asn Gly Leu Met Gly Arg
 225 230 235 240

Val Asp Glu Gly Val Asp Glu Phe Phe Thr Lys Lys Val Thr Lys Met
 245 250 255

Asp Ser Lys Lys Trp Ser Thr Arg Gly Ser Glu Ser His Glu Leu Asn
 260 265 270

Glu Gly Gly Asp Glu Lys Lys Lys Arg Asp Ser Arg Lys Ser Ser Gly
 275 280 285

Phe Leu Asn Leu Ile Lys Ser Arg Ser Lys Ser Glu Arg Pro Pro Thr
 290 295 300

Ile Leu Met Thr Glu Glu Pro Ser Ser Pro Lys Gly Ala Val Arg Ser
 305 310 315 320

Pro Pro Val Asp Cys Pro Arg Lys Asp Thr Lys Ala Ala Glu His Asn
 325 330 335

Gly Asn Ser Glu Arg Ile Glu Glu Ile Lys Thr Pro Asp Ser Phe Glu
 340 345 350

Glu Ser Gln Gly Glu Glu Ile Gly Lys Val Glu Arg Ser Asp Ser Lys
 355 360 365

Ser Ser Pro Gln Ala Gly Arg Arg Tyr Gly Val Gln Val Met Gly Ser
 370 375 380

Gly Leu Leu Ala Glu Met Lys Ala Lys Gln Glu Asn Arg Phe Gly Leu
 385 390 395 400

Gly Thr Pro Glu Lys Asn Thr Lys Ala Glu Pro Lys Ala Glu Ala Gly
 405 410 415

Ser Arg Ser Arg Ser Ser Ser Ser Thr Pro Thr Ser Pro Lys Pro Leu
 420 425 430

Leu Gln Ser Pro Lys Pro Ser Leu Ala Ala Arg Pro Val Ile Pro Gln
 435 440 445

Lys Pro Arg Thr Ala Ser Arg Pro Asp Asp Ile Pro Asp Ser Pro Ser
 450 455 460

Ser Pro Lys Val Ala Leu Leu Pro Pro Val Leu Lys Lys Val Pro Ser
 465 470 475 480

Asp Lys Glu Arg Asp Gly Gln Ser Ser Pro Gln Pro Ser Pro Arg Thr
 485 490 495

Phe Ser Gln Glu Val Ser Arg Arg Ser Trp Gly Gln Gln Ala Gln Glu
 500 505 510

Tyr Gln Glu Gln Lys Gln Arg Ser Ser Ser Lys Asp Gly His Gln Gly
 515 520 525

Ser Lys Ser Asn Asp Ser Gly Glu Glu Ala Glu Lys Glu Phe Ile Phe
 530 535 540

Val

545

<210> 148
 <211> 315
 <212> PRT
 <213> Human

<400> 148

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Met  Pro  Leu  Lys  Leu  Arg  Gly  Lys  Lys  Lys  Ala  Lys  Ser  Lys  Glu  Thr
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Ala  Gly  Leu  Val  Glu  Gly  Glu  Pro  Thr  Gly  Ala  Gly  Gly  Gly  Ser  Leu
20      25      30

Ser  Ala  Ser  Arg  Ala  Pro  Ala  Arg  Arg  Leu  Val  Phe  His  Ala  Gln  Leu
35      40      45

Ala  His  Gly  Ser  Ala  Thr  Gly  Arg  Val  Glu  Gly  Phe  Ser  Ser  Ile  Gln
50      55      60

Glu  Leu  Tyr  Ala  Gln  Ile  Ala  Gly  Ala  Phe  Glu  Ile  Ser  Pro  Ser  Glu
65      70      75      80

Ile  Leu  Tyr  Cys  Thr  Leu  Asn  Thr  Pro  Lys  Ile  Asp  Met  Glu  Arg  Leu
85      90      95

Leu  Gly  Gly  Gln  Leu  Gly  Leu  Glu  Asp  Phe  Ile  Phe  Ala  His  Val  Lys
100     105     110

Gly  Ile  Glu  Lys  Glu  Val  Asn  Val  Tyr  Lys  Ser  Glu  Asp  Ser  Leu  Gly
115     120     125

Leu  Thr  Ile  Thr  Asp  Asn  Gly  Val  Gly  Tyr  Ala  Phe  Ile  Lys  Arg  Ile
130     135     140

Lys  Asp  Gly  Gly  Val  Ile  Asp  Ser  Val  Lys  Thr  Ile  Cys  Val  Gly  Asp
145     150     155     160

His  Ile  Glu  Ser  Ile  Asn  Gly  Glu  Asn  Ile  Val  Gly  Trp  Arg  His  Tyr
165     170     175

Asp  Val  Ala  Lys  Lys  Leu  Lys  Glu  Leu  Lys  Lys  Glu  Glu  Leu  Phe  Thr
180     185     190

Met  Lys  Leu  Ile  Glu  Pro  Lys  Lys  Ala  Phe  Glu  Ile  Glu  Leu  Arg  Ser

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195 200 205
 Lys Ala Gly Lys Ser Ser Gly Glu Lys Ile Gly Cys Gly Arg Ala Thr
 210 215 220
 Leu Arg Leu Arg Ser Lys Gly Pro Ala Thr Val Glu Glu Met Pro Ser
 225 230 235 240
 Glu Thr Lys Ala Lys Ala Ile Glu Lys Ile Asp Asp Val Leu Glu Leu
 245 250 255
 Tyr Met Gly Ile Arg Asp Ile Asp Leu Ala Thr Thr Met Phe Glu Ala
 260 265 270
 Gly Lys Asp Lys Val Asn Pro Asp Glu Phe Ala Val Ala Leu Asp Glu
 275 280 285
 Thr Leu Gly Asp Phe Ala Phe Pro Asp Glu Phe Val Phe Asp Val Trp
 290 295 300
 Gly Val Ile Gly Asp Ala Lys Arg Arg Gly Leu
 305 310 315

 <210> 149
 <211> 486
 <212> PRT
 <213> Human

 <400> 149
 Met Pro Arg Pro Ala Pro Ala Arg Arg Leu Pro Gly Leu Leu Leu Leu
 1 5 10 15
 Leu Trp Pro Leu Leu Leu Leu Pro Ser Ala Ala Pro Asp Pro Val Ala
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 Arg Pro Gly Phe Arg Arg Leu Glu Thr Arg Gly Pro Gly Gly Ser Pro
 35 40 45
 Gly Arg Arg Pro Ser Pro Ala Ala Pro Asp Gly Ala Pro Ala Ser Gly
 50 55 60
 Thr Ser Glu Pro Gly Arg Ala Arg Gly Ala Gly Val Cys Lys Ser Arg
 65 70 75 80
 Pro Leu Asp Leu Val Phe Ile Ile Asp Ser Ser Arg Ser Val Arg Pro

					85					90					95
Leu	Glu	Phe	Thr	Lys	Val	Lys	Thr	Phe	Val	Ser	Arg	Ile	Ile	Asp	Thr
			100					105					110		
Leu	Asp	Ile	Gly	Pro	Ala	Asp	Thr	Arg	Val	Ala	Val	Val	Asn	Tyr	Ala
		115					120					125			
Ser	Thr	Val	Lys	Ile	Glu	Phe	Gln	Leu	Gln	Ala	Tyr	Thr	Asp	Lys	Gln
	130					135					140				
Ser	Leu	Lys	Gln	Ala	Val	Gly	Arg	Ile	Thr	Pro	Leu	Ser	Thr	Gly	Thr
145					150					155					160
Met	Ser	Gly	Leu	Ala	Ile	Gln	Thr	Ala	Met	Asp	Glu	Ala	Phe	Thr	Val
			165						170					175	
Glu	Ala	Gly	Ala	Arg	Glu	Pro	Ser	Ser	Asn	Ile	Pro	Lys	Val	Ala	Ile
			180					185					190		
Ile	Val	Thr	Asp	Gly	Arg	Pro	Gln	Asp	Gln	Val	Asn	Glu	Val	Ala	Ala
		195					200					205			
Arg	Ala	Gln	Ala	Ser	Gly	Ile	Glu	Leu	Tyr	Ala	Val	Gly	Val	Asp	Arg
	210					215					220				
Ala	Asp	Met	Ala	Ser	Leu	Lys	Met	Met	Ala	Ser	Glu	Pro	Leu	Glu	Glu
225					230					235				240	
His	Val	Phe	Tyr	Val	Glu	Thr	Tyr	Gly	Val	Ile	Glu	Lys	Leu	Ser	Ser
			245					250						255	
Arg	Phe	Gln	Glu	Thr	Phe	Cys	Ala	Leu	Asp	Pro	Cys	Val	Leu	Gly	Thr
		260						265					270		
His	Gln	Cys	Gln	His	Val	Cys	Ile	Ser	Asp	Gly	Glu	Gly	Lys	His	His
		275					280					285			
Cys	Glu	Cys	Ser	Gln	Gly	Tyr	Thr	Leu	Asn	Ala	Asp	Lys	Lys	Thr	Cys
	290					295					300				
Ser	Ala	Leu	Asp	Arg	Cys	Ala	Leu	Asn	Thr	His	Gly	Cys	Glu	His	Ile
305					310					315					320

Cys Val Asn Asp Arg Ser Gly Ser Tyr His Cys Glu Cys Tyr Glu Gly
 325 330 335

Tyr Thr Leu Asn Glu Asp Arg Lys Thr Cys Ser Ala Gln Asp Lys Cys
 340 345 350

Ala Leu Gly Thr His Gly Cys Gln His Ile Cys Val Asn Asp Arg Thr
 355 360 365

Gly Ser His His Cys Glu Cys Tyr Glu Gly Tyr Thr Leu Asn Ala Asp
 370 375 380

Lys Lys Thr Cys Ser Val Arg Asp Lys Cys Ala Leu Gly Ser His Gly
 385 390 395 400

Cys Gln His Ile Cys Val Ser Asp Gly Ala Ala Ser Tyr His Cys Asp
 405 410 415

Cys Tyr Pro Gly Tyr Thr Leu Asn Glu Asp Lys Lys Thr Cys Ser Ala
 420 425 430

Thr Glu Glu Ala Arg Arg Leu Val Ser Thr Glu Asp Ala Cys Gly Cys
 435 440 445

Glu Ala Thr Leu Ala Phe Gln Asp Lys Val Ser Ser Tyr Leu Gln Arg
 450 455 460

Leu Asn Thr Lys Leu Asp Asp Ile Leu Glu Lys Leu Lys Ile Asn Glu
 465 470 475 480

Tyr Gly Gln Ile His Arg
 485

<210> 150
 <211> 668
 <212> PRT
 <213> Human

<400> 150

Met Ala Ala Asn Met Tyr Arg Val Gly Asp Tyr Val Tyr Phe Glu Asn
 1 5 10 15

Ser Ser Ser Asn Pro Tyr Leu Val Arg Arg Ile Glu Glu Leu Asn Lys
 20 25 30

Thr Ala Asn Gly Asn Val Glu Ala Lys Val Val Cys Leu Phe Arg Arg
 35 40 45

Arg Asp Ile Ser Ser Ser Leu Asn Ser Leu Ala Asp Ser Asn Ala Arg
 50 55 60

Glu Phe Glu Glu Glu Ser Lys Gln Pro Gly Val Ser Glu Gln Gln Arg
 65 70 75 80

His Gln Leu Lys His Arg Glu Leu Phe Leu Ser Arg Gln Phe Glu Ser
 85 90 95

Leu Pro Ala Thr His Ile Arg Gly Lys Cys Ser Val Thr Leu Leu Asn
 100 105 110

Glu Thr Asp Ile Leu Ser Gln Tyr Leu Glu Lys Glu Asp Cys Phe Phe
 115 120 125

Tyr Ser Leu Val Phe Asp Pro Val Gln Lys Thr Leu Leu Ala Asp Gln
 130 135 140

Gly Glu Ile Arg Val Gly Cys Lys Tyr Gln Ala Glu Ile Pro Asp Arg
 145 150 155 160

Leu Val Glu Gly Glu Ser Asp Asn Arg Asn Gln Gln Lys Met Glu Met
 165 170 175

Lys Val Trp Asp Pro Asp Asn Pro Leu Thr Asp Arg Gln Ile Asp Gln
 180 185 190

Phe Leu Val Val Ala Arg Ala Val Gly Thr Phe Ala Arg Ala Leu Asp
 195 200 205

Cys Ser Ser Ser Ile Arg Gln Pro Ser Leu His Met Ser Ala Ala Ala
 210 215 220

Ala Ser Arg Asp Ile Thr Leu Phe His Ala Met Asp Thr Leu Gln Arg
 225 230 235 240

Asn Gly Tyr Asp Leu Ala Lys Ala Met Ser Thr Leu Val Pro Gln Gly
 245 250 255

Gly Pro Val Leu Cys Arg Asp Glu Met Glu Glu Trp Ser Ala Ser Glu
 260 265 270

Ala Met Leu Phe Glu Glu Ala Leu Glu Lys Tyr Gly Lys Asp Phe Asn
 275 280 285

Asp Ile Arg Gln Asp Phe Leu Pro Trp Lys Ser Leu Ala Ser Ile Val
 290 295 300

Gln Phe Tyr Tyr Met Trp Lys Thr Thr Asp Arg Tyr Ile Gln Gln Lys
 305 310 315 320

Arg Leu Lys Ala Ala Glu Ala Asp Ser Lys Leu Lys Gln Val Tyr Ile
 325 330 335

Pro Thr Tyr Thr Lys Pro Asn Pro Asn Gln Ile Ile Ser Val Gly Ser
 340 345 350

Lys Pro Gly Met Asn Gly Ala Gly Phe Gln Lys Gly Leu Thr Cys Glu
 355 360 365

Ser Cys His Thr Thr Gln Ser Ala Gln Trp Tyr Ala Trp Gly Pro Pro
 370 375 380

Asn Met Gln Cys Arg Leu Cys Ala Ser Cys Trp Ile Tyr Trp Lys Lys
 385 390 395 400

Tyr Gly Gly Leu Lys Thr Pro Thr Gln Leu Glu Gly Ala Thr Arg Gly
 405 410 415

Thr Thr Glu Pro His Ser Arg Gly His Leu Ser Arg Pro Glu Ala Gln
 420 425 430

Ser Leu Ser Pro Tyr Thr Thr Ser Ala Asn Arg Ala Lys Leu Leu Ala
 435 440 445

Lys Asn Arg Gln Thr Phe Leu Leu Gln Thr Thr Lys Leu Thr Arg Leu
 450 455 460

Ala Arg Arg Met Cys Arg Asp Leu Leu Gln Pro Arg Arg Ala Ala Arg
 465 470 475 480

Arg Pro Tyr Ala Pro Ile Asn Ala Asn Ala Ile Lys Ala Glu Cys Ser
 485 490 495

Ile Arg Leu Pro Lys Ala Ala Lys Thr Pro Leu Lys Ile His Pro Leu
 500 505 510

Val Arg Leu Pro Leu Ala Thr Ile Val Lys Asp Leu Val Ala Gln Ala
515 520 525

Pro Leu Lys Pro Lys Thr Pro Arg Gly Thr Lys Thr Pro Ile Asn Arg
530 535 540

Asn Gln Leu Ser Gln Asn Arg Gly Leu Gly Gly Ile Met Val Lys Arg
545 550 555 560

Ala Tyr Glu Thr Met Ala Gly Ala Gly Val Pro Phe Ser Ala Asn Gly
565 570 575

Arg Pro Leu Ala Ser Gly Ile Arg Ser Ser Ser Gln Pro Ala Ala Lys
580 585 590

Arg Gln Lys Leu Asn Pro Ala Asp Ala Pro Asn Pro Val Val Phe Val
595 600 605

Ala Thr Lys Asp Thr Arg Ala Leu Arg Lys Ala Leu Thr His Leu Glu
610 615 620

Met Arg Arg Ala Ala Arg Arg Pro Asn Leu Pro Leu Lys Val Lys Pro
625 630 635 640

Thr Leu Ile Ala Val Arg Pro Pro Val Pro Leu Pro Ala Pro Ser His
645 650 655

Pro Ala Ser Thr Asn Glu Pro Ile Val Leu Glu Asp
660 665

<210> 151
<211> 5179
<212> PRT
<213> Human

<400> 151

Met Gly Leu Pro Leu Ala Arg Leu Ala Ala Val Cys Leu Ala Leu Ser
1 5 10 15

Leu Ala Gly Gly Ser Glu Leu Gln Thr Glu Gly Arg Thr Arg Tyr His
20 25 30

Gly Arg Asn Val Cys Ser Thr Trp Gly Asn Phe His Tyr Lys Thr Phe
35 40 45

Asp Gly Asp Val Phe Arg Phe Pro Gly Leu Cys Asp Tyr Asn Phe Ala
50 55 60

Ser Asp Cys Arg Gly Ser Tyr Lys Glu Phe Ala Val His Leu Lys Arg
65 70 75 80

Gly Pro Gly Gln Ala Glu Ala Pro Ala Gly Val Glu Ser Ile Leu Leu
85 90 95

Thr Ile Lys Asp Asp Thr Ile Tyr Leu Thr Arg His Leu Ala Val Leu
100 105 110

Asn Gly Ala Val Val Ser Thr Pro His Tyr Ser Pro Gly Leu Leu Ile
115 120 125

Glu Lys Ser Asp Ala Tyr Thr Lys Val Tyr Ser Arg Ala Gly Leu Thr
130 135 140

Leu Met Trp Asn Arg Glu Asp Ala Leu Met Leu Glu Leu Asp Thr Lys
145 150 155 160

Phe Arg Asn His Thr Cys Gly Leu Cys Gly Asp Tyr Asn Gly Leu Gln
165 170 175

Ser Tyr Ser Glu Phe Leu Ser Asp Gly Val Leu Phe Ser Pro Leu Glu
180 185 190

Phe Gly Asn Met Gln Lys Ile Asn Gln Pro Asp Val Val Cys Glu Asp
195 200 205

Pro Glu Glu Glu Val Ala Pro Ala Ser Cys Ser Glu His Arg Ala Glu
210 215 220

Cys Glu Arg Leu Leu Thr Ala Glu Ala Phe Ala Asp Cys Gln Asp Leu
225 230 235 240

Val Pro Leu Glu Pro Tyr Leu Arg Ala Cys Gln Gln Asp Arg Cys Arg
245 250 255

Cys Pro Gly Gly Asp Thr Cys Val Cys Ser Thr Val Ala Glu Phe Ser
260 265 270

Arg Gln Cys Ser His Ala Gly Gly Arg Pro Gly Asn Trp Arg Thr Ala

275		280		285
Thr Leu Cys Pro Lys Thr Cys Pro Gly Asn Leu Val Tyr Leu Glu Ser				
290		295		300
Gly Ser Pro Cys Met Asp Thr Cys Ser His Leu Glu Val Ser Ser Leu				
305		310		315
				320
Cys Glu Glu His Arg Met Asp Gly Cys Phe Cys Pro Glu Gly Thr Val				
		325		330
				335
Tyr Asp Asp Ile Gly Asp Ser Gly Cys Val Pro Val Ser Gln Cys His				
		340		345
				350
Cys Arg Leu His Gly His Leu Tyr Thr Pro Gly Gln Glu Ile Thr Asn				
		355		360
				365
Asp Cys Glu Gln Cys Val Cys Asn Ala Gly Arg Trp Val Cys Lys Asp				
		370		375
				380
Leu Pro Cys Pro Gly Thr Cys Ala Leu Glu Gly Gly Ser His Ile Thr				
385		390		395
				400
Thr Phe Asp Gly Lys Thr Tyr Thr Phe His Gly Asp Cys Tyr Tyr Val				
		405		410
				415
Leu Ala Lys Gly Asp His Asn Asp Ser Tyr Ala Leu Leu Gly Glu Leu				
		420		425
				430
Ala Pro Cys Gly Ser Thr Asp Lys Gln Thr Cys Leu Lys Thr Val Val				
		435		440
				445
Leu Leu Ala Asp Lys Lys Lys Asn Ala Val Val Phe Lys Ser Asp Gly				
		450		455
				460
Ser Val Leu Leu Asn Gln Leu Gln Val Asn Leu Pro His Val Thr Ala				
465		470		475
				480
Ser Phe Ser Val Phe Arg Pro Ser Ser Tyr His Ile Met Val Ser Met				
		485		490
				495
Ala Ile Gly Val Arg Leu Gln Val Gln Leu Ala Pro Val Met Gln Leu				
		500		505
				510

Phe Val Thr Leu Asp Gln Ala Ser Gln Gly Gln Val Gln Gly Leu Cys
 515 520 525

Gly Asn Phe Asn Gly Leu Glu Gly Asp Asp Phe Lys Thr Ala Ser Gly
 530 535 540

Leu Val Glu Ala Thr Gly Ala Gly Phe Ala Asn Thr Trp Lys Ala Gln
 545 550 555 560

Ser Thr Cys His Asp Lys Leu Asp Trp Leu Asp Asp Pro Cys Ser Leu
 565 570 575

Asn Ile Glu Ser Ala Asn Tyr Ala Glu His Trp Cys Ser Leu Leu Lys
 580 585 590

Lys Thr Glu Thr Pro Phe Gly Arg Cys His Ser Ala Val Asp Pro Ala
 595 600 605

Glu Tyr Tyr Lys Arg Cys Lys Tyr Asp Thr Cys Asn Cys Gln Asn Asn
 610 615 620

Glu Asp Cys Leu Cys Ala Ala Leu Ser Ser Tyr Ala Arg Ala Cys Thr
 625 630 635 640

Ala Lys Gly Val Met Leu Trp Gly Trp Arg Glu His Val Cys Asn Lys
 645 650 655

Asp Val Gly Ser Cys Pro Asn Ser Gln Val Phe Leu Tyr Asn Leu Thr
 660 665 670

Thr Cys Gln Gln Thr Cys Arg Ser Leu Ser Glu Ala Asp Ser His Cys
 675 680 685

Leu Glu Gly Phe Ala Pro Val Asp Gly Cys Gly Cys Pro Asp His Thr
 690 695 700

Phe Leu Asp Glu Lys Gly Arg Cys Val Pro Leu Ala Lys Cys Ser Cys
 705 710 715 720

Tyr His Arg Gly Leu Tyr Leu Glu Ala Gly Asp Val Val Val Arg Gln
 725 730 735

Glu Glu Arg Cys Val Cys Arg Asp Gly Arg Leu His Cys Arg Gln Ile
 740 745 750

Protein 1: 1-1000 (1000 amino acids)

Arg Leu Ile Gly Gln Ser Cys Thr Ala Pro Lys Ile His Met Asp Cys
755 760 765

Ser Asn Leu Thr Ala Leu Ala Thr Ser Lys Pro Arg Ala Leu Ser Cys
770 775 780

Gln Thr Leu Ala Ala Gly Tyr Tyr His Thr Glu Cys Val Ser Gly Cys
785 790 795 800

Val Cys Pro Asp Gly Leu Met Asp Asp Gly Arg Gly Gly Cys Val Val
805 810 815

Glu Lys Glu Cys Pro Cys Val His Asn Asn Asp Leu Tyr Ser Ser Gly
820 825 830

Ala Lys Ile Lys Val Asp Cys Asn Thr Cys Thr Cys Lys Arg Gly Arg
835 840 845

Trp Val Cys Thr Gln Ala Val Cys His Gly Thr Cys Ser Ile Tyr Gly
850 855 860

Ser Gly His Tyr Ile Thr Phe Asp Gly Lys Tyr Tyr Asp Phe Asp Gly
865 870 875 880

His Cys Ser Tyr Val Ala Val Gln Asp Tyr Cys Gly Gln Asn Ser Ser
885 890 895

Leu Gly Ser Phe Ser Ile Ile Thr Glu Asn Val Pro Cys Gly Thr Thr
900 905 910

Gly Val Thr Cys Ser Lys Ala Ile Lys Ile Phe Met Gly Arg Thr Glu
915 920 925

Leu Lys Leu Glu Asp Lys His Arg Val Val Ile Gln Arg Asp Glu Gly
930 935 940

His His Val Ala Tyr Thr Thr Arg Glu Val Gly Gln Tyr Leu Val Val
945 950 955 960

Glu Ser Ser Thr Gly Ile Ile Val Ile Trp Asp Lys Arg Thr Thr Val
965 970 975

Phe Ile Lys Leu Ala Pro Ser Tyr Lys Gly Thr Val Cys Gly Leu Cys
980 985 990

FIG. 1 is a schematic diagram of the amino acid sequence of the protein of the present invention.

Gly Asn Phe Asp His Arg Ser Asn Asn Asp Phe Thr Thr Arg Asp His
995 1000 1005

Met Val Val Ser Ser Glu Leu Asp Phe Gly Asn Ser Trp Lys Glu
1010 1015 1020

Ala Pro Thr Cys Pro Asp Val Ser Thr Asn Pro Glu Pro Cys Ser
1025 1030 1035

Leu Asn Pro His Arg Arg Ser Trp Ala Glu Lys Gln Cys Ser Ile
1040 1045 1050

Leu Lys Ser Ser Val Phe Ser Ile Cys His Ser Lys Val Asp Pro
1055 1060 1065

Lys Pro Phe Tyr Glu Ala Cys Val His Asp Ser Cys Ser Cys Asp
1070 1075 1080

Thr Gly Gly Asp Cys Glu Cys Phe Cys Ser Ala Val Ala Ser Tyr
1085 1090 1095

Ala Gln Glu Cys Thr Lys Glu Gly Ala Cys Val Phe Trp Arg Thr
1100 1105 1110

Pro Asp Leu Cys Pro Ile Phe Cys Asp Tyr Tyr Asn Pro Pro His
1115 1120 1125

Glu Cys Glu Trp His Tyr Glu Pro Cys Gly Asn Arg Ser Phe Glu
1130 1135 1140

Thr Cys Arg Thr Ile Asn Gly Ile His Ser Asn Ile Ser Val Ser
1145 1150 1155

Tyr Leu Glu Gly Cys Tyr Pro Arg Cys Pro Lys Asp Arg Pro Ile
1160 1165 1170

Tyr Glu Glu Asp Leu Lys Lys Cys Val Thr Ala Asp Lys Cys Gly
1175 1180 1185

Cys Tyr Val Glu Asp Thr His Tyr Pro Pro Gly Ala Ser Val Pro
1190 1195 1200

Thr Glu Glu Thr Cys Lys Ser Cys Val Cys Thr Asn Ser Ser Gln

1215

Thr	Thr	Leu	Pro	Pro	Thr	Thr	Thr	Pro	Ser	Pro	Pro	Thr	Thr	Thr
1415						1420					1425			

Thr Thr Thr Pro Pro Pro Thr Thr Thr Pro Ser Pro Pro Ile Thr	1430	1435	1440
Thr Thr Thr Thr Pro Leu Pro Thr Thr Thr Pro Ser Pro Pro Ile	1445	1450	1455
Ser Thr Thr Thr Thr Pro Pro Pro Thr Thr Thr Pro Ser Pro Pro	1460	1465	1470
Thr Thr Thr Pro Ser Pro Pro Thr Thr Thr Pro Ser Pro Pro Thr	1475	1480	1485
Thr Thr Thr Thr Thr Pro Pro Pro Thr Thr Thr Pro Ser Pro Pro	1490	1495	1500
Met Thr Thr Pro Ile Thr Pro Pro Ala Ser Thr Thr Thr Leu Pro	1505	1510	1515
Pro Thr Thr Thr Pro Ser Pro Pro Thr Thr Thr Thr Thr Thr Pro	1520	1525	1530
Pro Pro Thr Thr Thr Pro Ser Pro Pro Thr Thr Thr Pro Ile Thr	1535	1540	1545
Pro Pro Thr Ser Thr Thr Thr Leu Pro Pro Thr Thr Thr Pro Ser	1550	1555	1560
Pro Pro Pro Thr Thr Thr Thr Thr Pro Pro Pro Thr Thr Thr Pro	1565	1570	1575
Ser Pro Pro Thr Thr Thr Thr Pro Ser Pro Pro Thr Ile Thr Thr	1580	1585	1590
Thr Thr Pro Pro Pro Thr Thr Thr Pro Ser Pro Pro Thr Thr Thr	1595	1600	1605
Thr Thr Thr Pro Pro Pro Thr Thr Thr Pro Ser Pro Pro Thr Thr	1610	1615	1620
Thr Pro Ile Thr Pro Pro Thr Ser Thr Thr Thr Leu Pro Pro Thr	1625	1630	1635
Thr Thr Pro Ser Pro Pro Pro Thr Thr Thr Thr Thr Pro Pro Pro	1640	1645	1650

Thr Thr Thr Pro Ser Pro Pro Thr Thr Thr Thr Pro Ser Pro Pro
 1655 1660 1665

 Ile Thr Thr Thr Thr Thr Pro Pro Pro Thr Thr Thr Pro Ser Ser
 1670 1675 1680

 Pro Ile Thr Thr Thr Pro Ser Pro Pro Thr Thr Thr Met Thr Thr
 1685 1690 1695

 Pro Ser Pro Thr Thr Thr Pro Ser Ser Pro Ile Thr Thr Thr Thr
 1700 1705 1710

 Thr Pro Ser Ser Thr Thr Thr Pro Ser Pro Pro Pro Thr Thr Met
 1715 1720 1725

 Thr Thr Pro Ser Pro Thr Thr Thr Pro Ser Pro Pro Thr Thr Thr
 1730 1735 1740

 Met Thr Thr Leu Pro Pro Thr Thr Thr Ser Ser Pro Leu Thr Thr
 1745 1750 1755

 Thr Pro Leu Pro Pro Ser Ile Thr Pro Pro Thr Phe Ser Pro Phe
 1760 1765 1770

 Ser Thr Thr Thr Pro Thr Thr Pro Cys Val Pro Leu Cys Asn Trp
 1775 1780 1785

 Thr Gly Trp Leu Asp Ser Gly Lys Pro Asn Phe His Lys Pro Gly
 1790 1795 1800

 Gly Asp Thr Glu Leu Ile Gly Asp Val Cys Gly Pro Gly Trp Ala
 1805 1810 1815

 Ala Asn Ile Ser Cys Arg Ala Thr Met Tyr Pro Asp Val Pro Ile
 1820 1825 1830

 Gly Gln Leu Gly Gln Thr Val Val Cys Asp Val Ser Val Gly Leu
 1835 1840 1845

 Ile Cys Lys Asn Glu Asp Gln Lys Pro Gly Gly Val Ile Pro Met
 1850 1855 1860

 Ala Phe Cys Leu Asn Tyr Glu Ile Asn Val Gln Cys Cys Glu Cys
 1865 1870 1875

Val Thr Gln Pro Thr Thr Met Thr Thr Thr Thr Thr Glu Asn Pro
 1880 1885 1890
 Thr Pro Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Thr Val Thr
 1895 1900 1905
 Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro
 1910 1915 1920
 Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly
 1925 1930 1935
 Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Thr Val
 1940 1945 1950
 Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Thr
 1955 1960 1965
 Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Thr
 1970 1975 1980
 Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Thr
 1985 1990 1995
 Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr
 2000 2005 2010
 Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr
 2015 2020 2025
 Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr
 2030 2035 2040
 Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr
 2045 2050 2055
 Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Thr
 2060 2065 2070
 Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr
 2075 2080 2085
 Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro

2090	2095	2100
Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro 2105 2110 2115		
Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Thr Pro Ile Thr Thr 2120 2125 2130		
Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr 2135 2140 2145		
Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr 2150 2155 2160		
Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Thr Pro Ile Thr 2165 2170 2175		
Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln 2180 2185 2190		
Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro 2195 2200 2205		
Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Thr Pro Ile 2210 2215 2220		
Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr 2225 2230 2235		
Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr 2240 2245 2250		
Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro 2255 2260 2265		
Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly 2270 2275 2280		
Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val 2285 2290 2295		
Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr 2300 2305 2310		

Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr
 2315 2320 2325

Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr
 2330 2335 2340

Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr
 2345 2350 2355

Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro
 2360 2365 2370

Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr
 2375 2380 2385

Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr
 2390 2395 2400

Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr
 2405 2410 2415

Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr
 2420 2425 2430

Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro
 2435 2440 2445

Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro
 2450 2455 2460

Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr
 2465 2470 2475

Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr
 2480 2485 2490

Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr
 2495 2500 2505

Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr
 2510 2515 2520

Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln
 2525 2530 2535

Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro
 2540 2545 2550
 Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile
 2555 2560 2565
 Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr
 2570 2575 2580
 Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr
 2585 2590 2595
 Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro
 2600 2605 2610
 Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly
 2615 2620 2625
 Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val
 2630 2635 2640
 Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr
 2645 2650 2655
 Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr
 2660 2665 2670
 Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr
 2675 2680 2685
 Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr
 2690 2695 2700
 Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro
 2705 2710 2715
 Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr
 2720 2725 2730
 Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr
 2735 2740 2745
 Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr
 2750 2755 2760

Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr
 2765 2770 2775

Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro
 2780 2785 2790

Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro
 2795 2800 2805

Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Thr Pro Ile Thr Thr
 2810 2815 2820

Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr
 2825 2830 2835

Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr
 2840 2845 2850

Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Thr Pro Ile Thr
 2855 2860 2865

Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln
 2870 2875 2880

Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro
 2885 2890 2895

Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile
 2900 2905 2910

Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr
 2915 2920 2925

Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr
 2930 2935 2940

Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro
 2945 2950 2955

Ile Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly
 2960 2965 2970

Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val

2975		2980		2985
Thr Pro	Thr Pro	Thr Pro	Thr Gly	Thr Gln
2990		2995		3000
Pro Ile	Thr Thr	Thr Thr	Thr Val	Thr Pro
3005		3010		3015
Gly Thr	Gln Thr	Pro Thr	Thr Thr	Pro Ile
3020		3025		3030
Val Thr	Pro Thr	Pro Thr	Thr Gly	Thr Gln
3035		3040		3045
Thr Pro	Ile Thr	Thr Thr	Thr Val	Thr Pro
3050		3055		3060
Thr Gly	Thr Gln	Thr Pro	Thr Thr	Pro Ile
3065		3070		3075
Thr Val	Thr Pro	Thr Pro	Thr Gly	Thr Gln
3080		3085		3090
Thr Thr	Pro Ile	Thr Thr	Thr Thr	Val Thr
3095		3100		3105
Pro Thr	Gly Thr	Gln Thr	Pro Thr	Thr Thr
3110		3115		3120
Thr Thr	Val Thr	Pro Thr	Pro Thr	Gly Thr
3125		3130		3135
Thr Thr	Thr Pro	Ile Thr	Thr Thr	Thr Val
3140		3145		3150
Thr Pro	Thr Gly	Thr Gln	Thr Pro	Thr Thr
3155		3160		3165
Thr Thr	Thr Val	Thr Pro	Thr Pro	Thr Gly
3170		3175		3180
Pro Thr	Thr Thr	Pro Ile	Thr Thr	Thr Thr
3185		3190		3195

Pro Thr	Pro Thr Gly Thr	Gln Thr	Pro Thr Thr Thr	Pro Ile Thr
3200		3205		3210
Thr Thr	Thr Thr Val Thr	Pro Thr	Pro Thr Pro Thr	Gly Thr Gln
3215		3220		3225
Thr Pro	Thr Thr Thr Pro	Ile Thr	Thr Thr Thr Thr	Val Thr Pro
3230		3235		3240
Thr Pro	Thr Pro Thr Gly	Thr Gln	Thr Pro Thr Thr	Thr Pro Ile
3245		3250		3255
Thr Thr	Thr Thr Thr Val	Thr Pro	Thr Pro Thr Pro	Thr Gly Thr
3260		3265		3270
Gln Thr	Pro Thr Thr Thr	Pro Ile	Thr Thr Thr Thr	Thr Val Thr
3275		3280		3285
Pro Thr	Pro Thr Pro Thr	Gly Thr	Gln Thr Pro Thr	Thr Thr Pro
3290		3295		3300
Ile Thr	Thr Thr Thr Thr	Val Thr	Pro Thr Pro Thr	Pro Thr Gly
3305		3310		3315
Thr Gln	Thr Pro Thr Thr	Thr Pro	Ile Thr Thr Thr	Thr Thr Val
3320		3325		3330
Thr Pro	Thr Pro Thr Pro	Thr Gly	Thr Gln Thr Pro	Thr Thr Thr
3335		3340		3345
Pro Ile	Thr Thr Thr Thr	Thr Val	Thr Pro Thr Pro	Thr Pro Thr
3350		3355		3360
Gly Thr	Gln Thr Pro Thr	Thr Thr	Pro Ile Thr Thr	Thr Thr Thr
3365		3370		3375
Val Thr	Pro Thr Pro Thr	Pro Thr	Gly Thr Gln Thr	Pro Thr Thr
3380		3385		3390
Thr Pro	Ile Thr Thr Thr	Thr Thr	Val Thr Pro Thr	Pro Thr Pro
3395		3400		3405
Thr Gly	Thr Gln Thr Pro	Thr Thr	Thr Pro Ile Thr	Thr Thr Thr
3410		3415		3420

Thr	Val	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Thr	Gln	Thr	Pro	Thr
3425						3430					3435			
Thr	Thr	Pro	Ile	Thr	Thr	Thr	Thr	Thr	Val	Thr	Pro	Thr	Pro	Thr
3440						3445					3450			
Pro	Thr	Gly	Thr	Gln	Thr	Pro	Thr	Thr	Thr	Pro	Ile	Thr	Thr	Thr
3455						3460					3465			
Thr	Thr	Val	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Thr	Gln	Thr	Pro
3470						3475					3480			
Thr	Thr	Thr	Pro	Ile	Thr	Thr	Thr	Thr	Thr	Val	Thr	Pro	Thr	Pro
3485						3490					3495			
Thr	Pro	Thr	Gly	Thr	Gln	Thr	Pro	Thr	Thr	Thr	Pro	Ile	Thr	Thr
3500						3505					3510			
Thr	Thr	Thr	Val	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Thr	Gln	Thr
3515						3520					3525			
Pro	Thr	Thr	Thr	Pro	Ile	Thr	Thr	Thr	Thr	Thr	Val	Thr	Pro	Thr
3530						3535					3540			
Pro	Thr	Pro	Thr	Gly	Thr	Gln	Thr	Pro	Thr	Thr	Thr	Pro	Ile	Thr
3545						3550					3555			
Thr	Thr	Thr	Thr	Val	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Thr	Gln
3560						3565					3570			
Thr	Pro	Thr	Thr	Thr	Pro	Ile	Thr	Thr	Thr	Thr	Thr	Val	Thr	Pro
3575						3580					3585			
Thr	Pro	Thr	Pro	Thr	Gly	Thr	Gln	Thr	Pro	Thr	Thr	Thr	Pro	Ile
3590						3595					3600			
Thr	Thr	Thr	Thr	Thr	Val	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Thr
3605						3610					3615			
Gln	Thr	Pro	Thr	Thr	Thr	Pro	Ile	Thr	Thr	Thr	Thr	Thr	Val	Thr
3620						3625					3630			
Pro	Thr	Pro	Thr	Pro	Thr	Gly	Thr	Gln	Thr	Pro	Thr	Thr	Thr	Pro
3635						3640					3645			

Ile	Thr	Thr	Thr	Thr	Thr	Val	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly
3650						3655							3660	
Thr	Gln	Thr	Pro	Thr	Thr	Thr	Pro	Ile	Thr	Thr	Thr	Thr	Thr	Val
3665						3670							3675	
Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Thr	Gln	Thr	Pro	Thr	Thr	Thr
3680						3685							3690	
Pro	Ile	Thr	Thr	Thr	Thr	Thr	Val	Thr	Pro	Thr	Pro	Thr	Pro	Thr
3695						3700							3705	
Gly	Thr	Gln	Thr	Pro	Thr	Thr	Thr	Pro	Ile	Thr	Thr	Thr	Thr	Thr
3710						3715							3720	
Val	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Thr	Gln	Thr	Pro	Thr	Thr
3725						3730							3735	
Thr	Pro	Ile	Thr	Thr	Thr	Thr	Thr	Val	Thr	Pro	Thr	Pro	Thr	Pro
3740						3745							3750	
Thr	Gly	Thr	Gln	Thr	Pro	Thr	Thr	Thr	Pro	Ile	Thr	Thr	Thr	Thr
3755						3760							3765	
Thr	Val	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Thr	Gln	Thr	Pro	Thr
3770						3775							3780	
Thr	Thr	Pro	Ile	Thr	Thr	Thr	Thr	Thr	Val	Thr	Pro	Thr	Pro	Thr
3785						3790							3795	
Pro	Thr	Gly	Thr	Gln	Thr	Pro	Thr	Thr	Thr	Pro	Ile	Thr	Thr	Thr
3800						3805							3810	
Thr	Thr	Val	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Thr	Gln	Thr	Pro
3815						3820							3825	
Thr	Thr	Thr	Pro	Ile	Thr	Thr	Thr	Thr	Thr	Val	Thr	Pro	Thr	Pro
3830						3835							3840	
Thr	Pro	Thr	Gly	Thr	Gln	Thr	Pro	Thr	Thr	Thr	Pro	Ile	Thr	Thr
3845						3850							3855	
Thr	Thr	Thr	Val	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Thr	Gln	Thr

3860	3865	3870
Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr 3875 3880 3885		
Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr 3890 3895 3900		
Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln 3905 3910 3915		
Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro 3920 3925 3930		
Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Thr Pro Ile 3935 3940 3945		
Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr 3950 3955 3960		
Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr 3965 3970 3975		
Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro 3980 3985 3990		
Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly 3995 4000 4005		
Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val 4010 4015 4020		
Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr 4025 4030 4035		
Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr 4040 4045 4050		
Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr 4055 4060 4065		
Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr 4070 4075 4080		

Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro
 4085 4090 4095

Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr
 4100 4105 4110

Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr
 4115 4120 4125

Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr
 4130 4135 4140

Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr
 4145 4150 4155

Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro
 4160 4165 4170

Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro
 4175 4180 4185

Thr Pro Thr Gly Thr Gln Thr Gly Pro Pro Thr His Thr Ser Thr
 4190 4195 4200

Ala Pro Ile Ala Glu Leu Thr Thr Ser Asn Pro Pro Pro Glu Ser
 4205 4210 4215

Ser Thr Pro Gln Thr Ser Arg Ser Thr Ser Ser Pro Leu Thr Glu
 4220 4225 4230

Ser Thr Thr Leu Leu Ser Thr Leu Pro Pro Ala Ile Glu Met Thr
 4235 4240 4245

Ser Thr Ala Pro Pro Ser Thr Pro Thr Ala Pro Thr Thr Thr Ser
 4250 4255 4260

Gly Gly His Thr Leu Ser Pro Pro Pro Ser Thr Thr Thr Ser Pro
 4265 4270 4275

Pro Gly Thr Pro Thr Arg Gly Thr Thr Thr Gly Ser Ser Ser Ala
 4280 4285 4290

Pro Thr Pro Ser Thr Val Gln Thr Thr Thr Thr Ser Ala Trp Thr
 4295 4300 4305

Pro Thr Pro Thr Pro Leu Ser Thr Pro Ser Ile Ile Arg Thr Thr
 4310 4315 4320

Gly Leu Arg Pro Tyr Pro Ser Ser Val Leu Ile Cys Cys Val Leu
 4325 4330 4335

Asn Asp Thr Tyr Tyr Ala Pro Gly Glu Glu Val Tyr Asn Gly Thr
 4340 4345 4350

Tyr Gly Asp Thr Cys Tyr Phe Val Asn Cys Ser Leu Ser Cys Thr
 4355 4360 4365

Leu Glu Phe Tyr Asn Trp Ser Cys Pro Ser Thr Pro Ser Pro Thr
 4370 4375 4380

Pro Thr Pro Ser Lys Ser Thr Pro Thr Pro Ser Lys Pro Ser Ser
 4385 4390 4395

Thr Pro Ser Lys Pro Thr Pro Gly Thr Lys Pro Pro Glu Cys Pro
 4400 4405 4410

Asp Phe Asp Pro Pro Arg Gln Glu Asn Glu Thr Trp Trp Leu Cys
 4415 4420 4425

Asp Cys Phe Met Ala Thr Cys Lys Tyr Asn Asn Thr Val Glu Ile
 4430 4435 4440

Val Lys Val Glu Cys Glu Pro Pro Pro Met Pro Thr Cys Ser Asn
 4445 4450 4455

Gly Leu Gln Pro Val Arg Val Glu Asp Pro Asp Gly Cys Cys Trp
 4460 4465 4470

His Trp Glu Cys Asp Cys Tyr Cys Thr Gly Trp Gly Asp Pro His
 4475 4480 4485

Tyr Val Thr Phe Asp Gly Leu Tyr Tyr Ser Tyr Gln Gly Asn Cys
 4490 4495 4500

Thr Tyr Val Leu Val Glu Glu Ile Ser Pro Ser Val Asp Asn Phe
 4505 4510 4515

Gly Val Tyr Ile Asp Asn Tyr His Cys Asp Pro Asn Asp Lys Val
 4520 4525 4530

Ser Cys	Pro Arg Thr Leu Ile	Val Arg His Glu Thr	Gln Glu Val
4535	4540	4545	
Leu Ile	Lys Thr Val His Met	Met Pro Met Gln Val	Gln Val Gln
4550	4555	4560	
Val Asn	Arg Gln Ala Val Ala	Leu Pro Tyr Lys Lys	Tyr Gly Leu
4565	4570	4575	
Glu Val	Tyr Gln Ser Gly Ile	Asn Tyr Val Val Asp	Ile Pro Glu
4580	4585	4590	
Leu Gly	Val Leu Val Ser Tyr	Asn Gly Leu Ser Phe	Ser Val Arg
4595	4600	4605	
Leu Pro	Tyr His Arg Phe Gly	Asn Asn Thr Lys Gly	Gln Cys Gly
4610	4615	4620	
Thr Cys	Thr Asn Thr Thr Ser	Asp Asp Cys Ile Leu	Pro Ser Gly
4625	4630	4635	
Glu Ile	Val Ser Asn Cys Glu	Ala Ala Ala Asp Gln	Trp Leu Val
4640	4645	4650	
Asn Asp	Pro Ser Lys Pro His	Cys Pro His Ser Ser	Ser Thr Thr
4655	4660	4665	
Lys Arg	Pro Ala Val Thr Val	Pro Gly Gly Gly Lys	Thr Thr Pro
4670	4675	4680	
His Lys	Asp Cys Thr Pro Ser	Pro Leu Cys Gln Leu	Ile Lys Asp
4685	4690	4695	
Ser Leu	Phe Ala Gln Cys His	Ala Leu Val Pro Pro	Gln His Tyr
4700	4705	4710	
Tyr Asp	Ala Cys Val Phe Asp	Ser Cys Phe Met Pro	Gly Ser Ser
4715	4720	4725	
Leu Glu	Cys Ala Ser Leu Gln	Ala Tyr Ala Ala Leu	Cys Ala Gln
4730	4735	4740	
Gln Asn	Ile Cys Leu Asp Trp	Arg Asn His Thr His	Gly Ala Cys

4745		4750		4755
Leu Val	Glu Cys Pro Ser	His Arg Glu Tyr Gln	Ala Cys Gly Pro	
4760		4765	4770	
Ala Glu	Glu Pro Thr Cys	Lys Ser Ser Ser Ser	Gln Gln Asn Asn	
4775		4780	4785	
Thr Val	Leu Val Glu Gly	Cys Phe Cys Pro Glu	Gly Thr Met Asn	
4790		4795	4800	
Tyr Ala	Pro Gly Phe Asp	Val Cys Val Lys Thr	Cys Gly Cys Val	
4805		4810	4815	
Gly Pro	Asp Asn Val Pro	Arg Glu Phe Gly Glu	His Phe Glu Phe	
4820		4825	4830	
Asp Cys	Lys Asn Cys Val	Cys Leu Glu Gly Gly	Ser Gly Ile Ile	
4835		4840	4845	
Cys Gln	Pro Lys Arg Cys	Ser Gln Lys Pro Val	Thr His Cys Val	
4850		4855	4860	
Glu Asp	Gly Thr Tyr Leu	Ala Thr Glu Val Asn	Pro Ala Asp Thr	
4865		4870	4875	
Cys Cys	Asn Ile Thr Val	Cys Lys Cys Asn Thr	Ser Leu Cys Lys	
4880		4885	4890	
Glu Lys	Pro Ser Val Cys	Pro Leu Gly Phe Glu	Val Lys Ser Lys	
4895		4900	4905	
Met Val	Pro Gly Arg Cys	Cys Pro Phe Tyr Trp	Cys Glu Ser Lys	
4910		4915	4920	
Gly Val	Cys Val His Gly	Asn Ala Glu Tyr Gln	Pro Gly Ser Pro	
4925		4930	4935	
Val Tyr	Ser Ser Lys Cys	Gln Asp Cys Val Cys	Thr Asp Lys Val	
4940		4945	4950	
Asp Asn	Asn Thr Leu Leu	Asn Val Ile Ala Cys	Thr His Val Pro	
4955		4960	4965	

Cys	Asn	Thr	Ser	Cys	Ser	Pro	Gly	Phe	Glu	Leu	Met	Glu	Ala	Pro
4970						4975					4980			
Gly	Glu	Cys	Cys	Lys	Lys	Cys	Glu	Gln	Thr	His	Cys	Ile	Ile	Lys
4985						4990					4995			
Arg	Pro	Asp	Asn	Gln	His	Val	Ile	Leu	Lys	Pro	Gly	Asp	Phe	Lys
5000						5005					5010			
Ser	Asp	Pro	Lys	Asn	Asn	Cys	Thr	Phe	Phe	Ser	Cys	Val	Lys	Ile
5015						5020					5025			
His	Asn	Gln	Leu	Ile	Ser	Ser	Val	Ser	Asn	Ile	Thr	Cys	Pro	Asn
5030						5035					5040			
Phe	Asp	Ala	Ser	Ile	Cys	Ile	Pro	Gly	Ser	Ile	Thr	Phe	Met	Pro
5045						5050					5055			
Asn	Gly	Cys	Cys	Lys	Thr	Cys	Thr	Pro	Arg	Asn	Glu	Thr	Arg	Val
5060						5065					5070			
Pro	Cys	Ser	Thr	Val	Pro	Val	Thr	Thr	Glu	Val	Ser	Tyr	Ala	Gly
5075						5080					5085			
Cys	Thr	Lys	Thr	Val	Leu	Met	Asn	His	Cys	Ser	Gly	Ser	Cys	Gly
5090						5095					5100			
Thr	Phe	Val	Met	Tyr	Ser	Ala	Lys	Ala	Gln	Ala	Leu	Asp	His	Ser
5105						5110					5115			
Cys	Ser	Cys	Cys	Lys	Glu	Glu	Lys	Thr	Ser	Gln	Arg	Glu	Val	Val
5120						5125					5130			
Leu	Ser	Cys	Pro	Asn	Gly	Gly	Ser	Leu	Thr	His	Thr	Tyr	Thr	His
5135						5140					5145			
Ile	Glu	Ser	Cys	Gln	Cys	Gln	Asp	Thr	Val	Cys	Gly	Leu	Pro	Thr
5150						5155					5160			
Gly	Thr	Ser	Arg	Arg	Ala	Arg	Arg	Ser	Pro	Arg	His	Leu	Gly	Ser
5165						5170					5175			
Gly														

<210> 152
 <211> 878
 <212> PRT
 <213> Human

<400> 152

Thr Ile Tyr Ser Thr Val Ser Ser Ser Thr Thr Ala Ile Thr Ser Pro
 1 5 10 15

Phe Thr Thr Ala Glu Thr Gly Val Thr Ser Thr Pro Ser Ser Pro Ser
 20 25 30

Ser Leu Ser Thr Asp Ile Pro Thr Thr Ser Leu Arg Thr Leu Thr Pro
 35 40 45

Leu Ser Leu Ser Thr Ser Thr Ser Leu Thr Thr Thr Thr Asp Leu Pro
 50 55 60

Ser Ile Pro Thr Asp Ile Ser Ser Leu Pro Thr Pro Ile His Ile Ile
 65 70 75 80

Ser Ser Ser Pro Ser Ile Gln Ser Thr Glu Thr Ser Ser Leu Val Gly
 85 90 95

Thr Thr Ser Pro Thr Met Ser Thr Val Arg Ala Thr Leu Arg Ser Thr
 100 105 110

Glu Asn Thr Pro Ile Ser Ser Phe Ser Thr Ser Ile Val Val Thr Pro
 115 120 125

Glu Thr Pro Thr Thr Gln Ala Pro Pro Val Leu Met Ser Ala Thr Gly
 130 135 140

Thr Gln Thr Ser Pro Val Pro Thr Thr Val Thr Phe Gly Ser Met Asp
 145 150 155 160

Ser Ser Thr Ser Thr Leu His Thr Leu Thr Pro Ser Thr Ala Leu Ser
 165 170 175

Lys Ile Met Ser Thr Ser Gln Phe Pro Ile Pro Ser Thr His Ser Ser
 180 185 190

Thr Leu Gln Thr Thr Pro Ser Ile Pro Ser Leu Gln Thr Ser Leu Thr
 195 200 205

Ser Thr Ser Glu Phe Thr Thr Glu Ser Phe Thr Arg Gly Ser Thr Ser
 210 215 220

Thr Asn Ala Ile Leu Thr Ser Phe Ser Thr Ile Ile Trp Ser Ser Thr
 225 230 235 240

Pro Thr Ile Ile Met Ser Ser Ser Pro Ser Ser Ala Ser Ile Thr Pro
 245 250 255

Val Phe Ala Thr Thr Ile His Ser Val Pro Ser Ser Pro Tyr Ile Phe
 260 265 270

Ser Thr Glu Asn Val Gly Ser Ala Ser Ile Thr Ala Phe Pro Ser Leu
 275 280 285

Ser Ser Ser Ser Thr Thr Ser Thr Ser Pro Thr Ser Ser Ser Leu Thr
 290 295 300

Thr Ala Leu Thr Glu Ile Thr Pro Phe Ser Tyr Ile Ser Leu Pro Ser
 305 310 315 320

Thr Thr Pro Cys Pro Gly Thr Ile Thr Ile Thr Ile Val Pro Ala Ser
 325 330 335

Pro Thr Asp Pro Cys Val Glu Met Asp Pro Ser Thr Glu Ala Thr Ser
 340 345 350

Pro Pro Thr Thr Pro Leu Thr Val Phe Pro Phe Thr Thr Glu Met Val
 355 360 365

Thr Cys Pro Ser Ser Ile Ser Met Gln Thr Thr Leu Ala Thr His Met
 370 375 380

Asp Thr Ser Ser Met Thr Pro Glu Ser Glu Ser Ser Ile Ile Pro Asn
 385 390 395 400

Ala Ser Ser Ser Thr Gly Thr Gly Thr Val Pro Thr Asn Thr Val Phe
 405 410 415

Thr Ser Thr Arg Leu Pro Thr Ser Glu Thr Trp Leu Ser Asn Asn Ser
 420 425 430

Val Ile Pro Thr Pro Leu Pro Gly Val Ser Thr Ile Pro Leu Thr Met
 435 440 445

Lys Pro Ser Ser Ser Leu Pro Thr Ile Leu Arg Thr Ser Ser Lys Ser
 450 455 460

Thr His Pro Ser Pro Pro Thr Ala Arg Thr Ser Glu Thr Ser Val Ala
 465 470 475 480

Thr Thr Gln Thr Pro Thr Thr Leu Thr Thr Arg Arg Thr Thr Pro Ile
 485 490 495

Thr Ser Trp Met Thr Thr Gln Ser Thr Leu Thr Thr Thr Ala Gly Thr
 500 505 510

Cys Asp Asn Gly Gly Thr Trp Glu Gln Gly Gln Cys Ala Cys Leu Pro
 515 520 525

Gly Phe Ser Gly Asp Arg Cys Gln Leu Gln Thr Arg Cys Gln Asn Gly
 530 535 540

Gly Gln Trp Asp Gly Leu Lys Cys Gln Cys Pro Ser Thr Phe Tyr Gly
 545 550 555 560

Ser Ser Cys Glu Phe Ala Val Glu Gln Val Asp Leu Asp Val Val Glu
 565 570 575

Thr Glu Val Gly Met Glu Val Ser Val Asp Gln Gln Phe Ser Pro Asp
 580 585 590

Leu Asn Asp Asn Thr Ser Gln Ala Tyr Arg Asp Phe Asn Lys Thr Phe
 595 600 605

Trp Asn Gln Met Gln Lys Ile Phe Ala Asp Met Gln Gly Phe Thr Phe
 610 615 620

Lys Gly Val Glu Ile Leu Ser Leu Arg Asn Gly Ser Ile Val Val Asp
 625 630 635 640

Tyr Leu Val Leu Leu Glu Met Pro Phe Ser Pro Gln Leu Glu Ser Glu
 645 650 655

Tyr Glu Gln Val Lys Thr Thr Leu Lys Glu Gly Leu Gln Asn Ala Ser
 660 665 670

Gln Asp Ala Asn Ser Cys Gln Asp Ser Gln Thr Leu Cys Phe Lys Pro

675

680

685

Asp Ser Ile Lys Val Asn Asn Asn Ser Lys Thr Glu Leu Thr Pro Glu
 690 695 700

Ala Ile Cys Arg Arg Ala Ala Pro Thr Gly Tyr Glu Glu Phe Tyr Phe
 705 710 715 720

Pro Leu Val Glu Ala Thr Arg Leu Arg Cys Val Thr Lys Cys Thr Ser
 725 730 735

Gly Val Asp Asn Ala Ile Asp Cys His Gln Gly Gln Cys Val Leu Glu
 740 745 750

Thr Ser Gly Pro Ala Cys Arg Cys Tyr Ser Thr Asp Thr His Trp Phe
 755 760 765

Ser Gly Pro Arg Cys Glu Val Ala Val His Trp Arg Ala Leu Val Gly
 770 775 780

Gly Leu Thr Ala Gly Ala Ala Leu Leu Val Leu Leu Leu Leu Ala Leu
 785 790 795 800

Gly Val Arg Ala Val Arg Ser Gly Trp Trp Gly Gly Gln Arg Arg Gly
 805 810 815

Arg Ser Trp Asp Gln Asp Arg Lys Trp Phe Glu Thr Trp Asp Glu Glu
 820 825 830

Val Val Gly Thr Phe Ser Asn Trp Gly Phe Glu Asp Asp Gly Thr Asp
 835 840 845

Lys Asp Thr Asn Phe His Val Ala Leu Glu Asn Val Asp Thr Thr Met
 850 855 860

Lys Val His Ile Lys Arg Pro Glu Met Thr Ser Ser Ser Val
 865 870 875

<210> 153
 <211> 1938
 <212> PRT
 <213> Human

<400> 153

Met Ser Ser Asp Ala Glu Met Ala Ile Phe Gly Glu Ala Ala Pro Tyr

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Leu Arg Lys Pro Glu Lys Glu Arg Ile Glu Ala Gln Asn Arg Pro Phe	20	25	30
Asp Ser Lys Lys Ala Cys Phe Val Ala Asp Asn Lys Glu Met Tyr Val	35	40	45
Lys Gly Met Ile Gln Thr Arg Glu Asn Asp Lys Val Ile Val Lys Thr	50	55	60
Leu Asp Asp Arg Met Leu Thr Leu Asn Asn Asp Gln Val Phe Pro Met	65	70	75
Asn Pro Pro Lys Phe Asp Lys Ile Glu Asp Met Ala Met Met Thr His	85	90	95
Leu His Glu Pro Ala Val Leu Tyr Asn Leu Lys Glu Arg Tyr Ala Ala	100	105	110
Trp Met Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Thr Val Asn Pro	115	120	125
Tyr Lys Trp Leu Pro Val Tyr Lys Pro Glu Val Val Ala Ala Tyr Arg	130	135	140
Gly Lys Lys Arg Gln Glu Ala Pro Pro His Ile Phe Ser Ile Ser Asp	145	150	155
Asn Ala Tyr Gln Phe Met Leu Thr Asp Arg Asp Asn Gln Ser Ile Leu	165	170	175
Ile Thr Gly Glu Ser Gly Ala Gly Lys Thr Val Asn Thr Lys Arg Val	180	185	190
Ile Gln Tyr Phe Ala Thr Ile Ala Val Thr Gly Asp Lys Lys Lys Glu	195	200	205
Thr Gln Pro Gly Lys Met Gln Gly Thr Leu Glu Asp Gln Ile Ile Gln	210	215	220
Ala Asn Pro Leu Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg Asn	225	230	235
			240

Asp Asn Ser Ser Arg Phe Gly Lys Phe Ile Arg Ile His Phe Gly Ala
 245 250 255
 Thr Gly Lys Leu Ala Ser Ala Asp Ile Glu Thr Tyr Leu Leu Glu Lys
 260 265 270
 Ser Arg Val Thr Phe Gln Leu Ser Ser Glu Arg Ser Tyr His Ile Phe
 275 280 285
 Tyr Gln Ile Met Ser Asn Lys Lys Pro Glu Leu Ile Asp Leu Leu Leu
 290 295 300
 Ile Ser Thr Asn Pro Phe Asp Phe Pro Phe Val Ser Gln Gly Glu Val
 305 310 315 320
 Thr Val Ala Ser Ile Asp Asp Ser Glu Glu Leu Leu Ala Thr Asp Asn
 325 330 335
 Ala Ile Asp Ile Leu Gly Phe Ser Ser Glu Glu Lys Val Gly Ile Tyr
 340 345 350
 Lys Leu Thr Gly Ala Val Met His Tyr Gly Asn Met Lys Phe Lys Gln
 355 360 365
 Lys Gln Arg Glu Glu Gln Ala Glu Pro Asp Gly Thr Glu Val Ala Asp
 370 375 380
 Lys Ala Gly Tyr Leu Met Gly Leu Asn Ser Ala Glu Met Leu Lys Gly
 385 390 395 400
 Leu Cys Cys Pro Arg Val Lys Val Gly Asn Glu Tyr Val Thr Lys Gly
 405 410 415
 Gln Asn Val Gln Gln Val Thr Asn Ser Val Gly Ala Leu Ala Lys Ala
 420 425 430
 Val Tyr Glu Lys Met Phe Leu Trp Met Val Thr Arg Ile Asn Gln Gln
 435 440 445
 Leu Asp Thr Lys Gln Pro Arg Gln Tyr Phe Ile Gly Val Leu Asp Ile
 450 455 460
 Ala Gly Phe Glu Ile Phe Asp Phe Asn Ser Leu Glu Gln Leu Cys Ile
 465 470 475 480

Asn Phe Thr Asn Glu Lys Leu Gln Gln Phe Phe Asn His His Met Phe
 485 490 495

Val Leu Glu Gln Glu Glu Tyr Lys Lys Glu Gly Ile Glu Trp Glu Phe
 500 505 510

Ile Asp Phe Gly Met Asp Leu Ala Ala Cys Ile Glu Leu Ile Glu Lys
 515 520 525

Pro Met Gly Ile Phe Ser Ile Leu Glu Glu Glu Cys Met Phe Pro Lys
 530 535 540

Ala Thr Asp Thr Ser Phe Lys Asn Lys Leu Tyr Asp Gln His Leu Gly
 545 550 555 560

Lys Ser Asn Asn Phe Gln Lys Pro Lys Pro Ala Lys Gly Lys Ala Glu
 565 570 575

Ala His Phe Ser Leu Val His Tyr Ala Gly Thr Val Asp Tyr Asn Ile
 580 585 590

Ala Gly Trp Leu Asp Lys Asn Lys Asp Pro Leu Asn Glu Thr Val Val
 595 600 605

Gly Leu Tyr Gln Lys Ser Ser Leu Lys Leu Leu Ser Phe Leu Phe Ser
 610 615 620

Asn Tyr Ala Gly Ala Glu Thr Gly Asp Ser Gly Gly Ser Lys Lys Gly
 625 630 635 640

Gly Lys Lys Lys Gly Ser Ser Phe Gln Thr Val Ser Ala Val Phe Arg
 645 650 655

Glu Asn Leu Asn Lys Leu Met Thr Asn Leu Arg Ser Thr His Pro His
 660 665 670

Phe Val Arg Cys Leu Ile Pro Asn Glu Thr Lys Thr Pro Gly Val Met
 675 680 685

Asp His Tyr Leu Val Met His Gln Leu Arg Cys Asn Gly Val Leu Glu
 690 695 700

Gly Ile Arg Ile Cys Arg Lys Gly Phe Pro Ser Arg Ile Leu Tyr Ala
 705 710 715 720

Asp Phe Lys Gln Arg Tyr Arg Ile Leu Asn Ala Ser Ala Ile Pro Glu
 725 730 735

Gly Gln Phe Ile Asp Ser Lys Asn Ala Ser Glu Lys Leu Leu Asn Ser
 740 745 750

Ile Asp Val Asp Arg Glu Gln Phe Arg Phe Gly Asn Thr Lys Val Phe
 755 760 765

Phe Lys Ala Gly Leu Leu Gly Leu Leu Glu Glu Met Arg Asp Glu Lys
 770 775 780

Leu Val Thr Leu Met Thr Ser Thr Gln Ala Val Cys Arg Gly Tyr Leu
 785 790 795 800

Met Arg Val Glu Phe Lys Lys Met Met Glu Arg Arg Asp Ser Ile Phe
 805 810 815

Cys Ile Gln Tyr Asn Ile Arg Ser Phe Met Asn Val Lys His Trp Pro
 820 825 830

Trp Met Asn Leu Phe Phe Lys Ile Lys Pro Leu Leu Lys Ser Ala Glu
 835 840 845

Ala Glu Lys Glu Met Ala Thr Met Lys Glu Asp Phe Glu Arg Thr Lys
 850 855 860

Glu Glu Leu Ala Arg Ser Glu Ala Arg Arg Lys Glu Leu Glu Glu Lys
 865 870 875 880

Met Val Ser Leu Leu Gln Glu Lys Asn Asp Leu Gln Leu Gln Val Gln
 885 890 895

Ser Glu Thr Glu Asn Leu Met Asp Ala Glu Glu Arg Cys Glu Gly Leu
 900 905 910

Ile Lys Ser Lys Ile Leu Leu Glu Ala Lys Val Lys Glu Leu Thr Glu
 915 920 925

Arg Leu Glu Glu Glu Glu Glu Met Asn Ser Glu Leu Val Ala Lys Lys
 930 935 940

Arg Asn Leu Glu Asp Lys Cys Ser Ser Leu Lys Arg Asp Ile Asp Asp

945		950		955		960
Leu Glu Leu Thr	Leu Thr Lys Val	Glu Lys Glu Lys	His Ala Thr Glu			
	965		970			975
Asn Lys Val Lys	Asn Leu Ser Glu	Glu Met Thr Ala	Leu Glu Glu Asn			
	980		985			990
Ile Ser Lys Leu	Thr Lys Glu Lys	Lys Ser Leu Gln	Glu Ala His Gln			
	995		1000			1005
Gln Thr Leu Asp	Asp Leu Gln Val	Glu Glu Asp Lys	Val Asn Gly			
	1010		1015			1020
Leu Ile Lys Ile	Asn Ala Lys Leu	Glu Gln Gln Thr	Asp Asp Leu			
	1025		1030			1035
Glu Gly Ser Leu	Glu Gln Glu Lys	Lys Leu Arg Ala	Asp Leu Glu			
	1040		1045			1050
Arg Ala Lys Arg	Lys Leu Glu Gly	Asp Leu Lys Met	Ser Gln Glu			
	1055		1060			1065
Ser Ile Met Asp	Leu Glu Asn Glu	Lys Gln Gln Ile	Glu Glu Lys			
	1070		1075			1080
Leu Lys Lys Lys	Glu Phe Glu Leu	Ser Gln Leu Gln	Ala Arg Ile			
	1085		1090			1095
Asp Asp Glu Gln	Val His Ser Leu	Gln Phe Gln Lys	Lys Lys Ile Lys			
	1100		1105			1110
Glu Leu Gln Ala	Arg Ile Glu Glu	Leu Glu Glu Glu	Glu Ile Glu Ala			
	1115		1120			1125
Glu His Thr Leu	Arg Ala Lys Ile	Glu Lys Gln Arg	Ser Asp Leu			
	1130		1135			1140
Ala Arg Glu Leu	Glu Glu Ile Ser	Glu Arg Leu Glu	Glu Ala Ser			
	1145		1150			1155
Gly Ala Thr Ser	Ala Gln Ile Glu	Met Asn Lys Lys	Arg Glu Ala			
	1160		1165			1170

Glu Phe	Gln Lys Met Arg Arg	Asp Leu Glu Glu Ala	Thr Leu Gln
1175	1180	1185	
His Glu	Ala Thr Ala Ala Thr	Leu Arg Lys Lys Gln	Ala Asp Ser
1190	1195	1200	
Val Ala	Glu Leu Gly Glu Gln	Ile Asp Asn Leu Gln	Arg Val Lys
1205	1210	1215	
Gln Lys	Leu Glu Lys Glu Lys	Ser Glu Leu Lys Met	Glu Ile Asp
1220	1225	1230	
Asp Met	Ala Ser Asn Ile Glu	Ala Leu Ser Lys Ser	Lys Ser Asn
1235	1240	1245	
Ile Glu	Arg Thr Cys Arg Thr	Val Glu Asp Gln Phe	Ser Glu Ile
1250	1255	1260	
Lys Ala	Lys Asp Glu Gln Gln	Thr Gln Leu Ile His	Asp Leu Asn
1265	1270	1275	
Met Gln	Lys Ala Arg Leu Gln	Thr Gln Asn Gly Glu	Leu Ser His
1280	1285	1290	
Arg Val	Glu Glu Lys Glu Ser	Leu Ile Ser Gln Leu	Thr Lys Ser
1295	1300	1305	
Lys Gln	Ala Leu Thr Gln Gln	Leu Glu Glu Leu Lys	Arg Gln Met
1310	1315	1320	
Glu Glu	Glu Thr Lys Ala Lys	Asn Ala Met Ala His	Ala Leu Gln
1325	1330	1335	
Ser Ser	Arg His Asp Cys Asp	Leu Leu Arg Glu Gln	Tyr Glu Glu
1340	1345	1350	
Glu Gln	Glu Ala Lys Ala Glu	Leu Gln Arg Ala Leu	Ser Lys Ala
1355	1360	1365	
Asn Ser	Glu Val Ala Gln Trp	Lys Thr Lys Tyr Glu	Thr Asp Ala
1370	1375	1380	
Ile Gln	Arg Thr Glu Glu Leu	Glu Glu Ala Lys Lys	Lys Leu Ala
1385	1390	1395	

Gln Arg	Leu Gln Glu Ala	Glu	Glu Lys Thr	Glu Thr	Ala Asn Ser
1400		1405		1410	
Lys Cys	Ala Ser Leu Glu	Lys	Thr Lys Gln Arg	Leu	Gln Gly Glu
1415		1420		1425	
Val Glu	Asp Leu Met Arg	Asp	Leu Glu Arg Ser	His	Thr Ala Cys
1430		1435		1440	
Ala Thr	Leu Asp Lys Lys	Gln	Arg Asn Phe Asp	Lys	Val Leu Ala
1445		1450		1455	
Glu Trp	Lys Gln Lys Leu	Asp	Glu Ser Gln Ala	Glu	Leu Glu Ala
1460		1465		1470	
Ala Gln	Lys Glu Ser Arg	Ser	Leu Ser Thr Glu	Leu	Phe Lys Met
1475		1480		1485	
Arg Asn	Ala Tyr Glu Glu	Val	Val Asp Gln Leu	Glu	Thr Leu Arg
1490		1495		1500	
Arg Glu	Asn Lys Asn Leu	Gln	Glu Glu Ile Ser	Asp	Leu Thr Glu
1505		1510		1515	
Gln Ile	Ala Glu Thr Gly	Lys	Asn Leu Gln Glu	Ala	Glu Lys Thr
1520		1525		1530	
Lys Lys	Leu Val Glu Gln	Glu	Lys Ser Asp Leu	Gln	Val Ala Leu
1535		1540		1545	
Glu Glu	Val Glu Gly Ser	Leu	Glu His Glu Glu	Ser	Lys Ile Leu
1550		1555		1560	
Arg Val	Gln Leu Glu Leu	Ser	Gln Val Lys Ser	Glu	Leu Asp Arg
1565		1570		1575	
Lys Val	Ile Glu Lys Asp	Glu	Glu Ile Glu Gln	Leu	Lys Arg Asn
1580		1585		1590	
Ser Gln	Arg Ala Ala Glu	Ala	Leu Gln Ser Val	Leu	Asp Ala Glu
1595		1600		1605	
Ile Arg	Ser Arg Asn Asp	Ala	Leu Arg Leu Lys	Lys	Lys Met Glu
1610		1615		1620	

Gly	Asp	Leu	Asn	Glu	Met	Glu	Ile	Gln	Leu	Gly	His	Ser	Asn	Arg
1625						1630					1635			
Gln	Met	Ala	Glu	Thr	Gln	Arg	His	Leu	Arg	Thr	Val	Gln	Gly	Gln
1640						1645					1650			
Leu	Lys	Asp	Ser	Gln	Leu	His	Leu	Asp	Asp	Ala	Leu	Arg	Ser	Asn
1655						1660					1665			
Glu	Asp	Leu	Lys	Glu	Gln	Leu	Ala	Ile	Val	Glu	Arg	Arg	Asn	Gly
1670						1675					1680			
Leu	Leu	Leu	Glu	Glu	Leu	Glu	Glu	Met	Lys	Val	Ala	Leu	Glu	Gln
1685						1690					1695			
Thr	Glu	Arg	Thr	Arg	Arg	Leu	Ser	Glu	Gln	Glu	Leu	Leu	Asp	Ala
1700						1705					1710			
Ser	Asp	Arg	Val	Gln	Leu	Leu	His	Ser	Gln	Asn	Thr	Ser	Leu	Ile
1715						1720					1725			
Asn	Thr	Lys	Lys	Lys	Leu	Glu	Ala	Asp	Ile	Ala	Gln	Cys	Gln	Ala
1730						1735					1740			
Glu	Val	Glu	Asn	Ser	Ile	Gln	Glu	Ser	Arg	Asn	Ala	Glu	Glu	Lys
1745						1750					1755			
Ala	Lys	Lys	Ala	Ile	Thr	Asp	Ala	Ala	Met	Met	Ala	Glu	Glu	Leu
1760						1765					1770			
Lys	Lys	Glu	Gln	Asp	Thr	Ser	Ala	His	Leu	Glu	Arg	Met	Lys	Lys
1775						1780					1785			
Asn	Leu	Glu	Gln	Thr	Val	Lys	Asp	Leu	Gln	His	Arg	Leu	Asp	Glu
1790						1795					1800			
Ala	Glu	Gln	Leu	Ala	Leu	Lys	Gly	Gly	Lys	Lys	Gln	Ile	Gln	Lys
1805						1810					1815			
Leu	Glu	Asn	Arg	Val	Arg	Glu	Leu	Glu	Asn	Glu	Leu	Asp	Val	Glu
1820						1825					1830			
Gln	Lys	Arg	Gly	Ala	Glu	Ala	Leu	Lys	Gly	Ala	His	Lys	Tyr	Glu

1835 1840 1845
 Arg Lys Val Lys Glu Met Thr Tyr Gln Ala Glu Glu Asp Arg Lys
 1850 1855 1860
 Asn Ile Leu Arg Leu Gln Asp Leu Val Asp Lys Leu Gln Ala Lys
 1865 1870 1875
 Val Lys Ser Tyr Lys Arg Gln Ala Glu Glu Ala Glu Glu Gln Ala
 1880 1885 1890
 Asn Thr Gln Leu Ser Arg Cys Arg Arg Val Gln His Glu Leu Glu
 1895 1900 1905
 Glu Ala Ala Glu Arg Ala Asp Ile Ala Glu Ser Gln Val Asn Lys
 1910 1915 1920
 Leu Arg Ala Lys Ser Arg Asp Val Gly Ser Gln Lys Met Glu Glu
 1925 1930 1935

 <210> 154
 <211> 173
 <212> PRT
 <213> Human

 <400> 154
 Met Ala Ser Arg Lys Thr Lys Lys Lys Glu Gly Gly Ala Leu Arg Ala
 1 5 10 15

 Gln Arg Ala Ser Ser Asn Val Phe Ser Asn Phe Glu Gln Thr Gln Ile
 20 25 30

 Gln Glu Phe Lys Glu Ala Phe Thr Leu Met Asp Gln Asn Arg Asp Gly
 35 40 45

 Phe Ile Asp Lys Glu Asp Leu Lys Asp Thr Tyr Ala Ser Leu Gly Lys
 50 55 60

 Thr Asn Val Lys Asp Asp Glu Leu Asp Ala Met Leu Lys Glu Ala Ser
 65 70 75 80

 Gly Pro Ile Asn Phe Thr Met Phe Leu Asn Leu Phe Gly Glu Lys Leu
 85 90 95

 Ser Gly Thr Asp Ala Glu Glu Thr Ile Leu Asn Ala Phe Lys Met Leu

100

105

110

Asp Pro Asp Gly Lys Gly Lys Ile Asn Lys Glu Tyr Ile Lys Arg Leu
 115 120 125

Leu Met Ser Gln Ala Asp Lys Met Thr Ala Glu Glu Val Asp Gln Met
 130 135 140

Phe Gln Phe Ala Ser Ile Asp Val Ala Gly Asn Leu Asp Tyr Lys Ala
 145 150 155 160

Leu Ser Tyr Val Ile Thr His Gly Glu Glu Lys Glu Glu
 165 170

<210> 155
 <211> 984
 <212> PRT
 <213> Human

<400> 155

Met Glu Thr Lys Gly Tyr His Ser Leu Pro Glu Gly Leu Asp Met Glu
 1 5 10 15

Arg Arg Trp Gly Gln Val Ser Gln Ala Val Glu Arg Ser Ser Leu Gly
 20 25 30

Pro Thr Glu Arg Thr Asp Glu Asn Asn Tyr Met Glu Ile Val Asn Val
 35 40 45

Ser Cys Val Ser Gly Ala Ile Pro Asn Asn Ser Thr Gln Gly Ser Ser
 50 55 60

Lys Glu Lys Gln Glu Leu Leu Pro Cys Leu Gln Gln Asp Asn Asn Arg
 65 70 75 80

Pro Gly Ile Leu Thr Ser Asp Ile Lys Thr Glu Leu Glu Ser Lys Glu
 85 90 95

Leu Ser Ala Thr Val Ala Gly Ser Met Gly Leu Tyr Met Asp Ser Val
 100 105 110

Arg Asp Ala Asp Tyr Ser Tyr Glu Gln Gln Asn Gln Gln Gly Ser Met
 115 120 125

Ser Pro Ala Lys Ile Tyr Gln Asn Val Glu Gln Leu Val Lys Phe Tyr

130		135		140
Lys Gly Asn Gly His Arg Pro Ser Thr Leu Ser Cys Val Asn Thr Pro				
145		150		155 160
Leu Arg Ser Phe Met Ser Asp Ser Gly Ser Ser Val Asn Gly Gly Val				
	165		170	175
Met Arg Ala Ile Val Lys Ser Pro Ile Met Cys His Glu Lys Ser Pro				
	180		185	190
Ser Val Cys Ser Pro Leu Asn Met Thr Ser Ser Val Cys Ser Pro Ala				
	195		200	205
Gly Ile Asn Ser Val Ser Ser Thr Thr Ala Ser Phe Gly Ser Phe Pro				
	210		215	220
Val His Ser Pro Ile Thr Gln Gly Thr Pro Leu Thr Cys Ser Pro Asn				
	225		230	235 240
Ala Glu Asn Arg Gly Ser Arg Ser His Ser Pro Ala His Ala Ser Asn				
	245		250	255
Val Gly Ser Pro Leu Ser Ser Pro Leu Ser Ser Met Lys Ser Ser Ile				
	260		265	270
Ser Ser Pro Pro Ser His Cys Ser Val Lys Ser Pro Val Ser Ser Pro				
	275		280	285
Asn Asn Val Thr Leu Arg Ser Ser Val Ser Ser Pro Ala Asn Ile Asn				
	290		295	300
Asn Ser Arg Cys Ser Val Ser Ser Pro Ser Asn Thr Asn Asn Arg Ser				
	305		310	315 320
Thr Leu Ser Ser Pro Ala Ala Ser Thr Val Gly Ser Ile Cys Ser Pro				
	325		330	335
Val Asn Asn Ala Phe Ser Tyr Thr Ala Ser Gly Thr Ser Ala Gly Ser				
	340		345	350
Ser Thr Leu Arg Asp Val Val Pro Ser Pro Asp Thr Gln Glu Lys Gly				
	355		360	365

Ala Gln Glu Val Pro Phe Pro Lys Thr Glu Glu Val Glu Ser Ala Ile
 370 375 380

Ser Asn Gly Val Thr Gly Gln Leu Asn Ile Val Gln Tyr Ile Lys Pro
 385 390 395 400

Glu Pro Asp Gly Ala Phe Ser Ser Ser Cys Leu Gly Gly Asn Ser Lys
 405 410 415

Ile Asn Ser Asp Ser Ser Phe Ser Val Pro Ile Lys Gln Glu Ser Thr
 420 425 430

Lys His Ser Cys Ser Gly Thr Ser Phe Lys Gly Asn Pro Thr Val Asn
 435 440 445

Pro Phe Pro Phe Met Asp Gly Ser Tyr Phe Ser Phe Met Asp Asp Lys
 450 455 460

Asp Tyr Tyr Ser Leu Ser Gly Ile Leu Gly Pro Pro Val Pro Gly Phe
 465 470 475 480

Asp Gly Asn Cys Glu Gly Ser Gly Phe Pro Val Gly Ile Lys Gln Glu
 485 490 495

Pro Asp Asp Gly Ser Tyr Tyr Pro Glu Ala Ser Ile Pro Ser Ser Ala
 500 505 510

Ile Val Gly Val Asn Ser Gly Gly Gln Ser Phe His Tyr Arg Ile Gly
 515 520 525

Ala Gln Gly Thr Ile Ser Leu Ser Arg Ser Ala Arg Asp Gln Ser Phe
 530 535 540

Gln His Leu Ser Ser Phe Pro Pro Val Asn Thr Leu Val Glu Ser Trp
 545 550 555 560

Lys Ser His Gly Asp Leu Ser Ser Arg Arg Ser Asp Gly Tyr Pro Val
 565 570 575

Leu Glu Tyr Ile Pro Glu Asn Val Ser Ser Ser Thr Leu Arg Ser Val
 580 585 590

Ser Thr Gly Ser Ser Arg Pro Ser Lys Ile Cys Leu Val Cys Gly Asp
 595 600 605

Glu Ala Ser Gly Cys His Tyr Gly Val Val Thr Cys Gly Ser Cys Lys
 610 615 620

Val Phe Phe Lys Arg Ala Val Glu Gly Gln His Asn Tyr Leu Cys Ala
 625 630 635 640

Gly Arg Asn Asp Cys Ile Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro
 645 650 655

Ala Cys Arg Leu Gln Lys Cys Leu Gln Ala Gly Met Asn Leu Gly Ala
 660 665 670

Arg Lys Ser Lys Lys Leu Gly Lys Leu Lys Gly Ile His Glu Glu Gln
 675 680 685

Pro Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Pro Gln Ser Pro
 690 695 700

Glu Glu Gly Thr Thr Tyr Ile Ala Pro Ala Lys Glu Pro Ser Val Asn
 705 710 715 720

Thr Ala Leu Val Pro Gln Leu Ser Thr Ile Ser Arg Ala Leu Thr Pro
 725 730 735

Ser Pro Val Met Val Leu Glu Asn Ile Glu Pro Glu Ile Val Tyr Ala
 740 745 750

Gly Tyr Asp Ser Ser Lys Pro Asp Thr Ala Glu Asn Leu Leu Ser Thr
 755 760 765

Leu Asn Arg Leu Ala Gly Lys Gln Met Ile Gln Val Val Lys Trp Ala
 770 775 780

Lys Val Leu Pro Gly Phe Lys Asn Leu Pro Leu Glu Asp Gln Ile Thr
 785 790 795 800

Leu Ile Gln Tyr Ser Trp Met Cys Leu Ser Ser Phe Ala Leu Ser Trp
 805 810 815

Arg Ser Tyr Lys His Thr Asn Ser Gln Phe Leu Tyr Phe Ala Pro Asp
 820 825 830

Leu Val Phe Asn Glu Glu Lys Met His Gln Ser Ala Met Tyr Glu Leu
 835 840 845

Cys Gln Gly Met His Gln Ile Ser Leu Gln Phe Val Arg Leu Gln Leu
850 855 860

Thr Phe Glu Glu Tyr Thr Ile Met Lys Val Leu Leu Leu Leu Ser Thr
865 870 875 880

Ile Pro Lys Asp Gly Leu Lys Ser Gln Ala Ala Phe Glu Glu Met Arg
885 890 895

Thr Asn Tyr Ile Lys Glu Leu Arg Lys Met Val Thr Lys Cys Pro Asn
900 905 910

Asn Ser Gly Gln Ser Trp Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu
915 920 925

Asp Ser Met His Asp Leu Val Ser Asp Leu Leu Glu Phe Cys Phe Tyr
930 935 940

Thr Phe Arg Glu Ser His Ala Leu Lys Val Glu Phe Pro Ala Met Leu
945 950 955 960

Val Glu Ile Ile Ser Asp Gln Leu Pro Lys Val Glu Ser Gly Asn Ala
965 970 975

Lys Pro Leu Tyr Phe His Arg Lys
980

<210> 156
<211> 495
<212> PRT
<213> Human

<400> 156

Met Ser Ser Asn Ser Asp Thr Gly Asp Leu Gln Glu Ser Leu Lys His
1 5 10 15

Gly Leu Thr Pro Ile Val Ser Gln Phe Lys Met Val Asn Tyr Ser Tyr
20 25 30

Asp Glu Asp Leu Glu Glu Leu Cys Pro Val Cys Gly Asp Lys Val Ser
35 40 45

Gly Tyr His Tyr Gly Leu Leu Thr Cys Glu Ser Cys Lys Gly Phe Phe
50 55 60

Lys Arg Thr Val Gln Asn Asn Lys Arg Tyr Thr Cys Ile Glu Asn Gln
65 70 75 80

Asn Cys Gln Ile Asp Lys Thr Gln Arg Lys Arg Cys Pro Tyr Cys Arg
85 90 95

Phe Gln Lys Cys Leu Ser Val Gly Met Lys Leu Glu Ala Val Arg Ala
100 105 110

Asp Arg Met Arg Gly Gly Arg Asn Lys Phe Gly Pro Met Tyr Lys Arg
115 120 125

Asp Arg Ala Leu Lys Gln Gln Lys Lys Ala Leu Ile Arg Ala Asn Gly
130 135 140

Leu Lys Leu Glu Ala Met Ser Gln Val Ile Gln Ala Met Pro Ser Asp
145 150 155 160

Leu Thr Ile Ser Ser Ala Ile Gln Asn Ile His Ser Ala Ser Lys Gly
165 170 175

Leu Pro Leu Asn His Ala Ala Leu Pro Pro Thr Asp Tyr Asp Arg Ser
180 185 190

Pro Phe Val Thr Ser Pro Ile Ser Met Thr Met Pro Pro His Gly Ser
195 200 205

Leu Gln Gly Tyr Gln Thr Tyr Gly His Phe Pro Ser Arg Ala Ile Lys
210 215 220

Ser Glu Tyr Pro Asp Pro Tyr Thr Ser Ser Pro Glu Ser Ile Met Gly
225 230 235 240

Tyr Ser Tyr Met Asp Ser Tyr Gln Thr Ser Ser Pro Ala Ser Ile Pro
245 250 255

His Leu Ile Leu Glu Leu Leu Lys Cys Glu Pro Asp Glu Pro Gln Val
260 265 270

Gln Ala Lys Ile Met Ala Tyr Leu Gln Gln Glu Gln Ala Asn Arg Ser
275 280 285

Lys His Glu Lys Leu Ser Thr Phe Gly Leu Met Cys Lys Met Ala Asp

290

295

300

Gln Thr Leu Phe Ser Ile Val Glu Trp Ala Arg Ser Ser Ile Phe Phe
 305 310 315 320

Arg Glu Leu Lys Val Asp Asp Gln Met Lys Leu Leu Gln Asn Cys Trp
 325 330 335

Ser Glu Leu Leu Ile Leu Asp His Ile Tyr Arg Gln Val Val His Gly
 340 345 350

Lys Glu Gly Ser Ile Phe Leu Val Thr Gly Gln Gln Val Asp Tyr Ser
 355 360 365

Ile Ile Ala Ser Gln Ala Gly Ala Thr Leu Asn Asn Leu Met Ser His
 370 375 380

Ala Gln Glu Leu Val Ala Lys Leu Arg Ser Leu Gln Phe Asp Gln Arg
 385 390 395 400

Glu Phe Val Cys Leu Lys Phe Leu Val Leu Phe Ser Leu Asp Val Lys
 405 410 415

Asn Leu Glu Asn Phe Gln Leu Val Glu Gly Val Gln Glu Gln Val Asn
 420 425 430

Ala Ala Leu Leu Asp Tyr Thr Met Cys Asn Tyr Pro Gln Gln Thr Glu
 435 440 445

Lys Phe Gly Gln Leu Leu Leu Arg Leu Pro Glu Ile Arg Ala Ile Ser
 450 455 460

Met Gln Ala Glu Glu Tyr Leu Tyr Tyr Lys His Leu Asn Gly Asp Val
 465 470 475 480

Pro Tyr Asn Asn Leu Leu Ile Glu Met Leu His Ala Lys Arg Ala
 485 490 495

<210> 157

<211> 2303

<212> PRT

<213> Human

<400> 157

Met Thr Ser Glu Glu Met Thr Ala Ser Val Leu Ile Pro Val Thr Gln

1	5	10	15
Arg Lys Val Val Ser Ala Gln Ser Ala Ala Asp Glu Ser Ser Glu Lys	20	25	30
Val Ser Asp Ile Asn Ile Ser Lys Ala His Thr Val Arg Arg Ser Gly	35	40	45
Glu Thr Ser His Thr Ile Ser Gln Leu Asn Lys Leu Lys Glu Glu Pro	50	55	60
Ser Gly Ser Asn Leu Pro Lys Ile Leu Ser Ile Ala Arg Glu Lys Ile	65	70	75
Val Ser Asp Glu Asn Ser Asn Glu Lys Cys Trp Glu Lys Ile Met Pro	85	90	95
Asp Ser Ala Lys Asn Leu Asn Ile Asn Cys Asn Asn Ile Leu Arg Asn	100	105	110
His Gln His Gly Leu Pro Gln Arg Gln Phe Tyr Glu Met Tyr Asn Ser	115	120	125
Val Ala Glu Glu Asp Leu Cys Leu Glu Thr Gly Ile Pro Ser Pro Leu	130	135	140
Glu Arg Lys Val Phe Pro Gly Ile Gln Leu Glu Leu Asp Arg Pro Ser	145	150	155
Met Gly Ile Ser Pro Leu Gly Asn Gln Ser Val Ile Ile Glu Thr Gly	165	170	175
Arg Ala His Pro Asp Ser Arg Arg Ala Val Phe His Phe His Tyr Glu	180	185	190
Val Asp Arg Arg Met Ser Asp Thr Phe Cys Thr Leu Ser Glu Asn Leu	195	200	205
Ile Leu Asp Asp Cys Gly Asn Cys Val Pro Leu Pro Gly Gly Glu Glu	210	215	220
Lys Gln Lys Lys Asn Tyr Val Ala Tyr Thr Cys Lys Leu Met Glu Leu	225	230	235
			240

Ala Lys Asn Cys Asp Asn Lys Asn Glu Gln Leu Gln Cys Asp His Cys
 245 250 255

Asp Thr Leu Asn Asp Lys Tyr Phe Cys Phe Glu Gly Ser Cys Glu Lys
 260 265 270

Val Asp Met Val Tyr Ser Gly Asp Ser Phe Cys Arg Lys Asp Phe Thr
 275 280 285

Asp Ser Gln Ala Ala Lys Thr Phe Leu Ser His Phe Glu Asp Phe Pro
 290 295 300

Asp Asn Cys Asp Asp Val Glu Glu Asp Ala Phe Lys Ser Lys Lys Glu
 305 310 315 320

Arg Ser Thr Leu Leu Val Arg Arg Phe Cys Lys Asn Asp Arg Glu Val
 325 330 335

Lys Lys Ser Val Tyr Thr Gly Thr Arg Ala Ile Val Arg Thr Leu Pro
 340 345 350

Ser Gly His Ile Gly Leu Thr Ala Trp Ser Tyr Ile Asp Gln Lys Arg
 355 360 365

Asn Gly Pro Leu Leu Pro Cys Gly Arg Val Met Glu Pro Pro Ser Thr
 370 375 380

Val Glu Ile Arg Gln Asp Gly Ser Gln Arg Leu Ser Glu Ala Gln Trp
 385 390 395 400

Tyr Pro Ile Tyr Asn Ala Val Arg Arg Glu Glu Thr Glu Asn Thr Val
 405 410 415

Gly Ser Leu Leu His Phe Leu Thr Lys Leu Pro Ala Ser Glu Thr Ala
 420 425 430

His Gly Arg Ile Ser Val Gly Pro Cys Leu Lys Gln Cys Val Arg Asp
 435 440 445

Thr Val Cys Glu Tyr Arg Ala Thr Leu Gln Arg Thr Ser Ile Ser Gln
 450 455 460

Tyr Ile Thr Gly Ser Leu Leu Glu Ala Thr Thr Ser Leu Gly Ala Arg
 465 470 475 480

Ser Gly Leu Leu Ser Thr Phe Gly Gly Ser Thr Gly Arg Met Met Leu
 485 490 495

Lys Glu Arg Gln Pro Gly Pro Ser Val Ala Asn Ser Asn Ala Leu Pro
 500 505 510

Ser Ser Ser Ala Gly Ile Ser Lys Glu Leu Ile Asp Leu Gln Pro Leu
 515 520 525

Ile Gln Phe Pro Glu Glu Val Ala Ser Ile Leu Met Glu Gln Glu Gln
 530 535 540

Thr Ile Tyr Arg Arg Val Leu Pro Val Asp Tyr Leu Cys Phe Leu Thr
 545 550 555 560

Arg Asp Leu Gly Thr Pro Glu Cys Gln Ser Ser Leu Pro Cys Leu Lys
 565 570 575

Ala Ser Ile Ser Ala Ser Ile Leu Thr Thr Gln Asn Gly Glu His Asn
 580 585 590

Ala Leu Glu Asp Leu Val Met Arg Phe Asn Glu Val Ser Ser Trp Val
 595 600 605

Thr Trp Leu Ile Leu Thr Ala Gly Ser Met Glu Glu Lys Arg Glu Val
 610 615 620

Phe Ser Tyr Leu Val His Val Ala Lys Cys Cys Trp Asn Met Gly Asn
 625 630 635 640

Tyr Asn Ala Val Met Glu Phe Leu Ala Gly Leu Arg Ser Arg Lys Val
 645 650 655

Leu Lys Met Trp Gln Phe Met Asp Gln Ser Asp Ile Glu Thr Met Arg
 660 665 670

Ser Leu Lys Asp Ala Met Ala Gln His Glu Ser Ser Cys Glu Tyr Arg
 675 680 685

Lys Val Val Thr Arg Ala Leu His Ile Pro Gly Cys Lys Val Val Pro
 690 695 700

Phe Cys Gly Val Phe Leu Lys Glu Leu Cys Glu Val' Leu Asp Gly Ala
 705 710 715 720

Ser Gly Leu Met Lys Leu Cys Pro Arg Tyr Asn Ser Gln Glu Glu Thr
 725 730 735

Leu Glu Phe Val Ala Asp Tyr Ser Gly Gln Asp Asn Phe Leu Gln Arg
 740 745 750

Val Gly Gln Asn Gly Leu Lys Asn Ser Glu Lys Glu Ser Thr Val Asn
 755 760 765

Ser Ile Phe Gln Val Ile Arg Ser Cys Asn Arg Ser Leu Glu Thr Asp
 770 775 780

Glu Glu Asp Ser Pro Ser Glu Gly Asn Ser Ser Arg Lys Ser Ser Leu
 785 790 795 800

Lys Asp Lys Ser Arg Trp Gln Phe Ile Ile Gly Asp Leu Leu Asp Ser
 805 810 815

Asp Asn Asp Ile Phe Glu Gln Ser Lys Glu Tyr Asp Ser His Gly Ser
 820 825 830

Glu Asp Ser Gln Lys Ala Phe Asp His Gly Thr Glu Leu Ile Pro Trp
 835 840 845

Tyr Val Leu Ser Ile Gln Ala Asp Val His Gln Phe Leu Leu Gln Gly
 850 855 860

Ala Thr Val Ile His Tyr Asp Gln Asp Thr His Leu Ser Ala Arg Cys
 865 870 875 880

Phe Leu Gln Leu Gln Pro Asp Asn Ser Thr Leu Thr Trp Val Lys Pro
 885 890 895

Thr Thr Ala Ser Pro Ala Ser Ser Lys Ala Lys Leu Gly Val Leu Asn
 900 905 910

Asn Thr Ala Glu Pro Gly Lys Phe Pro Leu Leu Gly Asn Ala Gly Leu
 915 920 925

Ser Ser Leu Thr Glu Gly Val Leu Asp Leu Phe Ala Val Lys Ala Val
 930 935 940

Tyr Met Gly His Pro Gly Ile Asp Ile His Thr Val Cys Val Gln Asn

945		950		955		960
Lys Leu Gly Ser Met Phe Leu Ser Glu Thr Gly Val Thr Leu Leu Tyr						
	965			970		975
Gly Leu Gln Thr Thr Asp Asn Arg Leu Leu His Phe Val Ala Pro Lys						
	980		985			990
His Thr Ala Lys Met Leu Phe Ser Gly Leu Leu Glu Leu Thr Arg Ala						
	995		1000			1005
Val Arg Lys Met Arg Lys Phe Pro Asp Gln Arg Gln Gln Trp Leu						
	1010		1015			1020
Arg Lys Gln Tyr Val Ser Leu Tyr Gln Glu Asp Gly Arg Tyr Glu						
	1025		1030			1035
Gly Pro Thr Leu Ala His Ala Val Glu Leu Phe Gly Gly Arg Arg						
	1040		1045			1050
Trp Ser Ala Arg Asn Pro Ser Pro Gly Thr Ser Ala Lys Asn Ala						
	1055		1060			1065
Glu Lys Pro Asn Met Gln Arg Asn Asn Thr Leu Gly Ile Ser Thr						
	1070		1075			1080
Thr Lys Lys Lys Lys Lys Ile Leu Met Arg Gly Glu Ser Gly Glu						
	1085		1090			1095
Val Thr Asp Asp Glu Met Ala Thr Arg Lys Ala Lys Met His Lys						
	1100		1105			1110
Glu Cys Arg Ser Arg Ser Gly Ser Asp Pro Gln Asp Ile Asn Glu						
	1115		1120			1125
Gln Glu Glu Ser Glu Val Asn Ala Ile Ala Asn Pro Pro Asn Pro						
	1130		1135			1140
Leu Pro Ser Arg Arg Ala His Ser Leu Thr Thr Ala Gly Ser Pro						
	1145		1150			1155
Asn Leu Ala Ala Gly Thr Ser Ser Pro Ile Arg Pro Val Ser Ser						
	1160		1165			1170

Pro Val Leu Ser Ser Ser Asn Lys Ser Pro Ser Ser Ala Trp Ser
 1175 1180 1185

 Ser Ser Ser Trp His Gly Arg Ile Lys Gly Gly Met Lys Gly Phe
 1190 1195 1200

 Gln Ser Phe Met Val Ser Asp Ser Asn Met Ser Phe Val Glu Phe
 1205 1210 1215

 Val Glu Leu Phe Lys Ser Phe Ser Val Arg Ser Arg Lys Asp Leu
 1220 1225 1230

 Lys Asp Leu Phe Asp Val Tyr Ala Val Pro Cys Asn Arg Ser Gly
 1235 1240 1245

 Ser Glu Ser Ala Pro Leu Tyr Thr Asn Leu Thr Ile Asp Glu Asn
 1250 1255 1260

 Thr Ser Asp Leu Gln Pro Asp Leu Asp Leu Leu Thr Arg Asn Val
 1265 1270 1275

 Ser Asp Leu Gly Leu Phe Ile Lys Ser Lys Gln Gln Leu Ser Asp
 1280 1285 1290

 Asn Gln Arg Gln Ile Ser Asp Ala Ile Ala Ala Ala Ser Ile Val
 1295 1300 1305

 Thr Asn Gly Thr Gly Ile Glu Ser Thr Ser Leu Gly Ile Phe Gly
 1310 1315 1320

 Val Gly Ile Leu Gln Leu Asn Asp Phe Leu Val Asn Cys Gln Gly
 1325 1330 1335

 Glu His Cys Thr Tyr Asp Glu Ile Leu Ser Ile Ile Gln Lys Phe
 1340 1345 1350

 Glu Pro Ser Ile Ser Met Cys His Gln Gly Leu Met Ser Phe Glu
 1355 1360 1365

 Gly Phe Ala Arg Phe Leu Met Asp Lys Glu Asn Phe Ala Ser Lys
 1370 1375 1380

 Asn Asp Glu Ser Gln Glu Asn Ile Lys Glu Leu Gln Leu Pro Leu
 1385 1390 1395

Ser Tyr Tyr Tyr Ile Glu Ser Ser His Asn Thr Tyr Leu Thr Gly
 1400 1405 1410
 His Gln Leu Lys Gly Glu Ser Ser Val Glu Leu Tyr Ser Gln Val
 1415 1420 1425
 Leu Leu Gln Gly Cys Arg Ser Val Glu Leu Asp Cys Trp Asp Gly
 1430 1435 1440
 Asp Asp Gly Met Pro Ile Ile Tyr His Gly His Thr Pro Thr Thr
 1445 1450 1455
 Lys Ile Pro Phe Lys Glu Val Val Glu Ala Ile Asp Arg Ser Ala
 1460 1465 1470
 Phe Ile Asn Ser Asp Leu Pro Ile Ile Ile Ser Ile Glu Asn His
 1475 1480 1485
 Cys Ser Leu Pro Gln Gln Arg Lys Met Ala Glu Ile Phe Lys Thr
 1490 1495 1500
 Val Phe Gly Glu Lys Leu Val Thr Lys Phe Leu Phe Glu Thr Asp
 1505 1510 1515
 Phe Ser Asp Asp Pro Met Leu Pro Ser Pro Asp Gln Leu Arg Lys
 1520 1525 1530
 Lys Val Leu Leu Lys Asn Lys Lys Leu Lys Ala His Gln Thr Pro
 1535 1540 1545
 Val Asp Ile Leu Lys Gln Lys Ala His Gln Leu Ala Ser Met Gln
 1550 1555 1560
 Val Gln Ala Tyr Asn Gly Gly Asn Ala Asn Pro Arg Pro Ala Asn
 1565 1570 1575
 Asn Glu Glu Glu Glu Asp Glu Glu Asp Glu Tyr Asp Tyr Asp Tyr
 1580 1585 1590
 Glu Ser Leu Ser Asp Asp Asn Ile Leu Glu Asp Arg Pro Glu Asn
 1595 1600 1605
 Lys Ser Cys Asn Asp Lys Leu Gln Phe Glu Tyr Asn Glu Glu Ile
 1610 1615 1620

Pro Lys Arg Ile Lys Lys Ala Asp Asn Ser Ala Cys Asn Lys Gly
 1625 1630 1635

 Lys Val Tyr Asp Met Glu Leu Gly Glu Glu Phe Tyr Leu Asp Gln
 1640 1645 1650

 Asn Lys Lys Glu Ser Arg Gln Ile Ala Pro Glu Leu Ser Asp Leu
 1655 1660 1665

 Val Ile Tyr Arg Gln Ala Val Lys Phe Pro Gly Leu Ser Thr Leu
 1670 1675 1680

 Asn Ala Ser Gly Ser Ser Arg Gly Lys Glu Arg Lys Ser Arg Lys
 1685 1690 1695

 Ser Ile Phe Gly Asn Asn Pro Gly Arg Met Ser Pro Gly Glu Thr
 1700 1705 1710

 Ala Ser Phe Asn Lys Thr Ser Gly Lys Ser Ser Cys Glu Gly Ile
 1715 1720 1725

 Arg Gln Thr Trp Glu Glu Ser Ser Ser Pro Leu Asn Pro Thr Thr
 1730 1735 1740

 Ser Leu Ser Ala Ile Ile Arg Thr Pro Lys Cys Tyr His Ile Ser
 1745 1750 1755

 Ser Leu Asn Glu Asn Ala Ala Lys Arg Leu Cys Arg Arg Tyr Ser
 1760 1765 1770

 Gln Lys Leu Ile Gln His Thr Ala Cys Gln Leu Leu Arg Thr Tyr
 1775 1780 1785

 Pro Ala Ala Thr Arg Ile Asp Ser Ser Asn Pro Asn Pro Leu Met
 1790 1795 1800

 Phe Trp Leu His Gly Ile Gln Leu Val Ala Leu Asn Tyr Gln Thr
 1805 1810 1815

 Asp Asp Leu Pro Leu His Leu Asn Ala Ala Met Phe Glu Ala Asn
 1820 1825 1830

 Gly Gly Cys Gly Tyr Val Leu Lys Pro Pro Val Leu Trp Asp Lys

1835		1840		1845
Asn Cys Pro Met Tyr Gln Lys Phe Ser Pro Leu Glu Arg Asp Leu				
1850		1855		1860
Asp Ser Met Asp Pro Ala Val Tyr Ser Leu Thr Ile Val Ser Gly				
1865		1870		1875
Gln Asn Val Cys Pro Ser Asn Ser Met Gly Ser Pro Cys Ile Glu				
1880		1885		1890
Val Asp Val Leu Gly Met Pro Leu Asp Ser Cys His Phe Arg Thr				
1895		1900		1905
Lys Pro Ile His Arg Asn Thr Leu Asn Pro Met Trp Asn Glu Gln				
1910		1915		1920
Phe Leu Phe Arg Val His Phe Glu Asp Leu Val Phe Leu Arg Phe				
1925		1930		1935
Ala Val Val Glu Asn Asn Ser Ser Ala Val Thr Ala Gln Arg Ile				
1940		1945		1950
Ile Pro Leu Lys Ala Leu Lys Arg Gly Tyr Arg His Leu Gln Leu				
1955		1960		1965
Arg Asn Leu His Asn Glu Val Leu Glu Ile Ser Ser Leu Phe Ile				
1970		1975		1980
Asn Ser Arg Arg Met Glu Glu Asn Ser Ser Gly Asn Thr Met Ser				
1985		1990		1995
Ala Ser Ser Met Phe Asn Thr Glu Glu Arg Lys Cys Leu Gln Thr				
2000		2005		2010
His Arg Val Thr Val His Gly Val Pro Gly Pro Glu Pro Phe Thr				
2015		2020		2025
Val Phe Thr Ile Asn Gly Gly Thr Lys Ala Lys Gln Leu Leu Gln				
2030		2035		2040
Gln Ile Leu Thr Asn Glu Gln Asp Ile Lys Pro Val Thr Thr Asp				
2045		2050		2055

Tyr	Phe	Leu	Met	Glu	Glu	Lys	Tyr	Phe	Ile	Ser	Lys	Glu	Lys	Asn
2060						2065					2070			
Glu	Cys	Arg	Lys	Gln	Pro	Phe	Gln	Arg	Ala	Ile	Gly	Pro	Glu	Glu
2075						2080					2085			
Glu	Ile	Met	Gln	Ile	Leu	Ser	Ser	Trp	Phe	Pro	Glu	Glu	Gly	Tyr
2090						2095					2100			
Met	Gly	Arg	Ile	Val	Leu	Lys	Thr	Gln	Gln	Glu	Asn	Leu	Glu	Glu
2105						2110					2115			
Lys	Asn	Ile	Val	Gln	Asp	Asp	Lys	Glu	Val	Ile	Leu	Ser	Ser	Glu
2120						2125					2130			
Glu	Glu	Ser	Phe	Phe	Val	Gln	Val	His	Asp	Val	Ser	Pro	Glu	Gln
2135						2140					2145			
Pro	Arg	Thr	Val	Ile	Lys	Ala	Pro	Arg	Val	Ser	Thr	Ala	Gln	Asp
2150						2155					2160			
Val	Ile	Gln	Gln	Thr	Leu	Cys	Lys	Ala	Lys	Tyr	Ser	Tyr	Ser	Ile
2165						2170					2175			
Leu	Ser	Asn	Pro	Asn	Pro	Ser	Asp	Tyr	Val	Leu	Leu	Glu	Glu	Val
2180						2185					2190			
Val	Lys	Asp	Thr	Thr	Asn	Lys	Lys	Thr	Thr	Thr	Pro	Lys	Ser	Ser
2195						2200					2205			
Gln	Arg	Val	Leu	Leu	Asp	Gln	Glu	Cys	Val	Phe	Gln	Ala	Gln	Ser
2210						2215					2220			
Lys	Trp	Lys	Gly	Ala	Gly	Lys	Phe	Ile	Leu	Lys	Leu	Lys	Glu	Gln
2225						2230					2235			
Val	Gln	Ala	Ser	Arg	Glu	Asp	Lys	Lys	Lys	Gly	Ile	Ser	Phe	Ala
2240						2245					2250			
Ser	Glu	Leu	Lys	Lys	Leu	Thr	Lys	Ser	Thr	Lys	Gln	Pro	Arg	Gly
2255						2260					2265			
Leu	Thr	Ser	Pro	Ser	Gln	Leu	Leu	Thr	Ser	Glu	Ser	Ile	Gln	Thr
2270						2275					2280			

Lys Glu Glu Lys Pro Val Gly Gly Leu Ser Pro Val Thr Gln Trp
 2285 2290 2295

Ile Thr Asp Ser Asp
 2300

<210> 158
 <211> 303
 <212> PRT
 <213> Human

<400> 158

Met Ala Ser Trp Ala Lys Gly Arg Ser Tyr Leu Ala Pro Gly Leu Leu
 1 5 10 15

Gln Gly Gln Val Ala Ile Val Thr Gly Gly Ala Thr Gly Ile Gly Lys
 20 25 30

Ala Ile Val Lys Glu Leu Leu Glu Leu Gly Ser Asn Val Val Ile Ala
 35 40 45

Ser Arg Lys Leu Glu Arg Leu Lys Ser Ala Ala Asp Glu Leu Gln Ala
 50 55 60

Asn Leu Pro Pro Thr Lys Gln Ala Arg Val Ile Pro Ile Gln Cys Asn
 65 70 75 80

Ile Arg Asn Glu Glu Glu Val Asn Asn Leu Val Lys Ser Thr Leu Asp
 85 90 95

Thr Phe Gly Lys Ile Asn Phe Leu Val Asn Asn Gly Gly Gly Gln Phe
 100 105 110

Leu Ser Pro Ala Glu His Ile Ser Ser Lys Gly Trp His Ala Val Leu
 115 120 125

Glu Thr Asn Leu Thr Gly Thr Phe Tyr Met Cys Lys Ala Val Tyr Ser
 130 135 140

Ser Trp Met Lys Glu His Gly Gly Ser Ile Val Asn Ile Ile Val Pro
 145 150 155 160

Thr Lys Ala Gly Phe Pro Leu Ala Val His Ser Gly Ala Ala Arg Ala
 165 170 175

Gly Val Tyr Asn Leu Thr Lys Ser Leu Ala Leu Glu Trp Ala Cys Ser
 180 185 190

Gly Ile Arg Ile Asn Cys Val Ala Pro Gly Val Ile Tyr Ser Gln Thr
 195 200 205

Ala Val Glu Asn Tyr Gly Ser Trp Gly Gln Ser Phe Phe Glu Gly Ser
 210 215 220

Phe Gln Lys Ile Pro Ala Lys Arg Ile Gly Val Pro Glu Glu Val Ser
 225 230 235 240

Ser Val Val Cys Phe Leu Leu Ser Pro Ala Ala Ser Phe Ile Thr Gly
 245 250 255

Gln Ser Val Asp Val Asp Gly Gly Arg Ser Leu Tyr Thr His Ser Tyr
 260 265 270

Glu Val Pro Asp His Asp Asn Trp Pro Lys Gly Ala Gly Asp Leu Ser
 275 280 285

Val Val Lys Lys Met Lys Glu Thr Phe Lys Glu Lys Ala Lys Leu
 290 295 300

<210> 159
 <211> 246
 <212> PRT
 <213> Human

<400> 159

Met Glu Glu Ala Lys Ser Gln Ser Leu Glu Glu Asp Phe Glu Gly Gln
 1 5 10 15

Ala Thr His Thr Gly Pro Lys Gly Val Ile Asn Asp Trp Arg Lys Phe
 20 25 30

Lys Leu Glu Ser Gln Asp Ser Asp Ser Ile Pro Pro Ser Lys Lys Glu
 35 40 45

Ile Leu Arg Gln Met Ser Ser Pro Gln Ser Arg Asn Gly Lys Asp Ser
 50 55 60

Lys Glu Arg Val Ser Arg Lys Met Ser Ile Gln Glu Tyr Glu Leu Ile
 65 70 75 80

His Lys Glu Lys Glu Asp Glu Asn Cys Leu Arg Lys Tyr Arg Arg Gln
 85 90 95

Cys Met Gln Asp Met His Gln Lys Leu Ser Phe Gly Pro Arg Tyr Gly
 100 105 110

Phe Val Tyr Glu Leu Glu Thr Gly Lys Gln Phe Leu Glu Thr Ile Glu
 115 120 125

Lys Glu Leu Lys Ile Thr Thr Ile Val Val His Ile Tyr Glu Asp Gly
 130 135 140

Ile Lys Gly Cys Asp Ala Leu Asn Ser Ser Leu Thr Cys Leu Ala Ala
 145 150 155 160

Glu Tyr Pro Ile Val Lys Phe Cys Lys Ile Lys Ala Ser Asn Thr Gly
 165 170 175

Ala Gly Asp Arg Phe Ser Leu Asp Val Leu Pro Thr Leu Leu Ile Tyr
 180 185 190

Lys Gly Gly Glu Leu Ile Ser Asn Phe Ile Ser Val Ala Glu Gln Phe
 195 200 205

Ala Glu Glu Phe Phe Ala Gly Asp Val Glu Ser Phe Leu Asn Glu Tyr
 210 215 220

Gly Leu Leu Pro Glu Arg Glu Val His Val Leu Glu His Thr Lys Ile
 225 230 235 240

Glu Glu Glu Asp Val Glu
 245

<210> 160
 <211> 403
 <212> PRT
 <213> Human

<400> 160

Met Thr Ala Ile Ile Lys Glu Ile Val Ser Arg Asn Lys Arg Arg Tyr
 1 5 10 15

Gln Glu Asp Gly Phe Asp Leu Asp Leu Thr Tyr Ile Tyr Pro Asn Ile
 20 25 30

Ile Ala Met Gly Phe Pro Ala Glu Arg Leu Glu Gly Val Tyr Arg Asn
 35 40 45
 Asn Ile Asp Asp Val Val Arg Phe Leu Asp Ser Lys His Lys Asn His
 50 55 60
 Tyr Lys Ile Tyr Asn Leu Cys Ala Glu Arg His Tyr Asp Thr Ala Lys
 65 70 75 80
 Phe Asn Cys Arg Val Ala Gln Tyr Pro Phe Glu Asp His Asn Pro Pro
 85 90 95
 Gln Leu Glu Leu Ile Lys Pro Phe Cys Glu Asp Leu Asp Gln Trp Leu
 100 105 110
 Ser Glu Asp Asp Asn His Val Ala Ala Ile His Cys Lys Ala Gly Lys
 115 120 125
 Gly Arg Thr Gly Val Met Ile Cys Ala Tyr Leu Leu His Arg Gly Lys
 130 135 140
 Phe Leu Lys Ala Gln Glu Ala Leu Asp Phe Tyr Gly Glu Val Arg Thr
 145 150 155 160
 Arg Asp Lys Lys Gly Val Thr Ile Pro Ser Gln Arg Arg Tyr Val Tyr
 165 170 175
 Tyr Tyr Ser Tyr Leu Leu Lys Asn His Leu Asp Tyr Arg Pro Val Ala
 180 185 190
 Leu Leu Phe His Lys Met Met Phe Glu Thr Ile Pro Met Phe Ser Gly
 195 200 205
 Gly Thr Cys Asn Pro Gln Phe Val Val Cys Gln Leu Lys Val Lys Ile
 210 215 220
 Tyr Ser Ser Asn Ser Gly Pro Thr Arg Arg Glu Asp Lys Phe Met Tyr
 225 230 235 240
 Phe Glu Phe Pro Gln Pro Leu Pro Val Cys Gly Asp Ile Lys Val Glu
 245 250 255
 Phe Phe His Lys Gln Asn Lys Met Leu Lys Lys Asp Lys Met Phe His
 260 265 270

Phe Trp Val Asn Thr Phe Phe Ile Pro Gly Pro Glu Glu Thr Ser Glu
275 280 285

Lys Val Glu Asn Gly Ser Leu Cys Asp Gln Glu Ile Asp Ser Ile Cys
290 295 300

Ser Ile Glu Arg Ala Asp Asn Asp Lys Glu Tyr Leu Val Leu Thr Leu
305 310 315 320

Thr Lys Asn Asp Leu Asp Lys Ala Asn Lys Asp Lys Ala Asn Arg Tyr
325 330 335

Phe Ser Pro Asn Phe Lys Val Lys Leu Tyr Phe Thr Lys Thr Val Glu
340 345 350

Glu Pro Ser Asn Pro Glu Ala Ser Ser Ser Thr Ser Val Thr Pro Asp
355 360 365

Val Ser Asp Asn Glu Pro Asp His Tyr Arg Tyr Ser Asp Thr Thr Asp
370 375 380

Ser Asp Pro Glu Asn Glu Pro Phe Asp Glu Asp Gln His Thr Gln Ile
385 390 395 400

Thr Lys Val

<210> 161
<211> 336
<212> PRT
<213> Human

<400> 161

Met Leu Gln Ser Leu Ala Gly Ser Ser Cys Val Arg Leu Val Glu Arg
1 5 10 15

His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu Leu
20 25 30

Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro Tyr
35 40 45

Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe Leu
50 55 60

Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu Gly
 65 70 75 80

Arg Val Leu Glu Ala Ser Asn Tyr Gly Val Ser Val Leu Ser Asn Ala
 85 90 95

Ser Gly Asn Trp Asn Trp Asp Phe Thr Ser Ala Leu Phe Phe Ala Ser
 100 105 110

Thr Val Leu Ser Thr Thr Gly Tyr Gly His Thr Val Pro Leu Ser Asp
 115 120 125

Gly Gly Lys Ala Phe Cys Ile Ile Tyr Ser Val Ile Gly Ile Pro Phe
 130 135 140

Thr Leu Leu Phe Leu Thr Ala Val Val Gln Arg Ile Thr Val His Val
 145 150 155 160

Thr Arg Arg Pro Val Leu Tyr Phe His Ile Arg Trp Gly Phe Ser Lys
 165 170 175

Gln Val Val Ala Ile Val His Ala Val Leu Leu Gly Phe Val Thr Val
 180 185 190

Ser Cys Phe Phe Phe Ile Pro Ala Ala Val Phe Ser Val Leu Glu Asp
 195 200 205

Asp Trp Asn Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu Ser
 210 215 220

Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn Gln Lys
 225 230 235 240

Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Leu Gly
 245 250 255

Leu Ile Ala Met Leu Val Val Leu Glu Thr Phe Cys Glu Leu His Glu
 260 265 270

Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp Glu
 275 280 285

Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser Ile

290

295

300

Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu Pro
 305 310 315 320

Phe Val Ala Thr Gln Ser Ser Ala Cys Val Asp Gly Pro Ala Asn His
 325 330 335

<210> 162
 <211> 604
 <212> PRT
 <213> Human

<400> 162

Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu Ala Leu Ser His
 1 5 10 15

Thr Ala Asn Pro Cys Cys Ser His Pro Cys Gln Asn Arg Gly Val Cys
 20 25 30

Met Ser Val Gly Phe Asp Gln Tyr Lys Cys Asp Cys Thr Arg Thr Gly
 35 40 45

Phe Tyr Gly Glu Asn Cys Ser Thr Pro Glu Phe Leu Thr Arg Ile Lys
 50 55 60

Leu Phe Leu Lys Pro Thr Pro Asn Thr Val His Tyr Ile Leu Thr His
 65 70 75 80

Phe Lys Gly Phe Trp Asn Val Val Asn Asn Ile Pro Phe Leu Arg Asn
 85 90 95

Ala Ile Met Ser Tyr Val Leu Thr Ser Arg Ser His Leu Ile Asp Ser
 100 105 110

Pro Pro Thr Tyr Asn Ala Asp Tyr Gly Tyr Lys Ser Trp Glu Ala Phe
 115 120 125

Ser Asn Leu Ser Tyr Tyr Thr Arg Ala Leu Pro Pro Val Pro Asp Asp
 130 135 140

Cys Pro Thr Pro Leu Gly Val Lys Gly Lys Lys Gln Leu Pro Asp Ser
 145 150 155 160

Asn Glu Ile Val Glu Lys Leu Leu Leu Arg Arg Lys Phe Ile Pro Asp

	165		170		175
Pro Gln Gly Ser Asn Met Met Phe Ala Phe Phe Ala Gln His Phe Thr	180		185		190
His Gln Phe Phe Lys Thr Asp His Lys Arg Gly Pro Ala Phe Thr Asn	195		200		205
Gly Leu Gly His Gly Val Asp Leu Asn His Ile Tyr Gly Glu Thr Leu	210		215		220
Ala Arg Gln Arg Lys Leu Arg Leu Phe Lys Asp Gly Lys Met Lys Tyr	225		230		235
Gln Ile Ile Asp Gly Glu Met Tyr Pro Pro Thr Val Lys Asp Thr Gln	245		250		255
Ala Glu Met Ile Tyr Pro Pro Gln Val Pro Glu His Leu Arg Phe Ala	260		265		270
Val Gly Gln Glu Val Phe Gly Leu Val Pro Gly Leu Met Met Tyr Ala	275		280		285
Thr Ile Trp Leu Arg Glu His Asn Arg Val Cys Asp Val Leu Lys Gln	290		295		300
Glu His Pro Glu Trp Gly Asp Glu Gln Leu Phe Gln Thr Ser Arg Leu	305		310		315
Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Asp Tyr Val Gln	325		330		335
His Leu Ser Gly Tyr His Phe Lys Leu Lys Phe Asp Pro Glu Leu Leu	340		345		350
Phe Asn Lys Gln Phe Gln Tyr Gln Asn Arg Ile Ala Ala Glu Phe Asn	355		360		365
Thr Leu Tyr His Trp His Pro Leu Leu Pro Asp Thr Phe Gln Ile His	370		375		380
Asp Gln Lys Tyr Asn Tyr Gln Gln Phe Ile Tyr Asn Asn Ser Ile Leu	385		390		395
					400

Leu Glu His Gly Ile Thr Gln Phe Val Glu Ser Phe Thr Arg Gln Ile
 405 410 415

Ala Gly Arg Val Ala Gly Gly Arg Asn Val Pro Pro Ala Val Gln Lys
 420 425 430

Val Ser Gln Ala Ser Ile Asp Gln Ser Arg Gln Met Lys Tyr Gln Ser
 435 440 445

Phe Asn Glu Tyr Arg Lys Arg Phe Met Leu Lys Pro Tyr Glu Ser Phe
 450 455 460

Glu Glu Leu Thr Gly Glu Lys Glu Met Ser Ala Glu Leu Glu Ala Leu
 465 470 475 480

Tyr Gly Asp Ile Asp Ala Val Glu Leu Tyr Pro Ala Leu Leu Val Glu
 485 490 495

Lys Pro Arg Pro Asp Ala Ile Phe Gly Glu Thr Met Val Glu Val Gly
 500 505 510

Ala Pro Phe Ser Leu Lys Gly Leu Met Gly Asn Val Ile Cys Ser Pro
 515 520 525

Ala Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Gln Ile
 530 535 540

Ile Asn Thr Ala Ser Ile Gln Ser Leu Ile Cys Asn Asn Val Lys Gly
 545 550 555 560

Cys Pro Phe Thr Ser Phe Ser Val Pro Asp Pro Glu Leu Ile Lys Thr
 565 570 575

Val Thr Ile Asn Ala Ser Ser Ser Arg Ser Gly Leu Asp Asp Ile Asn
 580 585 590

Pro Thr Val Leu Leu Lys Glu Arg Ser Thr Glu Leu
 595 600

<210> 163
 <211> 117
 <212> PRT
 <213> Human

<400> 163

Met Arg Ala Ser Ser Phe Leu Ile Val Val Val Phe Leu Ile Ala Gly
1 5 10 15

Thr Leu Val Leu Glu Ala Ala Val Thr Gly Val Pro Val Lys Gly Gln
20 25 30

Asp Thr Val Lys Gly Arg Val Pro Phe Asn Gly Gln Asp Pro Val Lys
35 40 45

Gly Gln Val Ser Val Lys Gly Gln Asp Lys Val Lys Ala Gln Glu Pro
50 55 60

Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys Pro Ile Ile Leu
65 70 75 80

Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys Leu Lys Asp Thr
85 90 95

Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser Cys Gly Met Ala
100 105 110

Cys Phe Val Pro Gln
115

<210> 164
<211> 464
<212> PRT
<213> Human

<400> 164

Met Ala Gly Gln Asp Pro Ala Leu Ser Thr Ser His Pro Phe Tyr Asp
1 5 10 15

Val Ala Arg His Gly Ile Leu Gln Val Ala Gly Asp Asp Arg Phe Gly
20 25 30

Arg Arg Val Val Thr Phe Ser Cys Cys Arg Met Pro Pro Ser His Glu
35 40 45

Leu Asp His Gln Arg Leu Leu Glu Tyr Leu Lys Tyr Thr Leu Asp Gln
50 55 60

Tyr Val Glu Asn Asp Tyr Thr Ile Val Tyr Phe His Tyr Gly Leu Asn
65 70 75 80

Ser Arg Asn Lys Pro Ser Leu Gly Trp Leu Gln Ser Ala Tyr Lys Glu
 85 90 95

Phe Asp Arg Lys Asp Gly Asp Leu Thr Met Trp Pro Arg Leu Val Ser
 100 105 110

Asn Ser Lys Leu Lys Arg Ser Ser His Leu Ser Leu Pro Lys Tyr Trp
 115 120 125

Asp Tyr Arg Tyr Lys Lys Asn Leu Lys Ala Leu Tyr Val Val His Pro
 130 135 140

Thr Ser Phe Ile Lys Val Leu Trp Asn Ile Leu Lys Pro Leu Ile Ser
 145 150 155 160

His Lys Phe Gly Lys Lys Val Ile Tyr Phe Asn Tyr Leu Ser Glu Leu
 165 170 175

His Glu His Leu Lys Tyr Asp Gln Leu Val Ile Pro Pro Glu Val Leu
 180 185 190

Arg Tyr Asp Glu Lys Leu Gln Ser Leu His Glu Gly Arg Thr Pro Pro
 195 200 205

Pro Thr Lys Thr Pro Pro Pro Arg Pro Pro Leu Pro Thr Gln Gln Phe
 210 215 220

Gly Val Ser Leu Gln Tyr Leu Lys Asp Lys Asn Gln Gly Glu Leu Ile
 225 230 235 240

Pro Pro Val Leu Arg Phe Thr Val Thr Tyr Leu Arg Glu Lys Gly Leu
 245 250 255

Arg Thr Glu Gly Leu Phe Arg Arg Ser Ala Ser Val Gln Thr Val Arg
 260 265 270

Glu Ile Gln Arg Leu Tyr Asn Gln Gly Lys Pro Val Asn Phe Asp Asp
 275 280 285

Tyr Gly Asp Ile His Ile Pro Ala Val Ile Leu Lys Thr Phe Leu Arg
 290 295 300

Glu Leu Pro Gln Pro Leu Leu Thr Phe Gln Ala Tyr Glu Gln Ile Leu
 305 310 315 320

Gly Ile Thr Cys Val Glu Ser Ser Leu Arg Val Thr Gly Cys Arg Gln
 325 330 335

Ile Leu Arg Ser Leu Pro Glu His Asn Tyr Val Val Leu Arg Tyr Leu
 340 345 350

Met Gly Phe Leu His Ala Val Ser Arg Glu Ser Ile Phe Asn Lys Met
 355 360 365

Asn Ser Ser Asn Leu Ala Cys Val Phe Gly Leu Asn Leu Ile Trp Pro
 370 375 380

Ser Gln Gly Val Ser Ser Leu Ser Ala Leu Val Pro Leu Asn Met Phe
 385 390 395 400

Thr Glu Leu Leu Ile Glu Tyr Tyr Glu Lys Ile Phe Ser Thr Pro Glu
 405 410 415

Ala Pro Gly Glu His Gly Leu Ala Pro Trp Glu Gln Gly Ser Arg Ala
 420 425 430

Ala Pro Leu Gln Glu Ala Val Pro Arg Thr Gln Ala Thr Gly Leu Thr
 435 440 445

Lys Pro Thr Leu Pro Pro Ser Pro Leu Met Ala Ala Arg Arg Arg Leu
 450 455 460

<210> 165
 <211> 156
 <212> PRT
 <213> Human

<400> 165

Met Ala Leu Glu Lys Ser Leu Val Arg Leu Leu Leu Leu Val Leu Ile
 1 5 10 15

Leu Leu Val Leu Gly Trp Val Gln Pro Ser Leu Gly Lys Glu Ser Arg
 20 25 30

Ala Lys Lys Phe Gln Arg Gln His Met Asp Ser Asp Ser Ser Pro Ser
 35 40 45

Ser Ser Ser Thr Tyr Cys Asn Gln Met Met Arg Arg Arg Asn Met Thr
 50 55 60

Gln Gly Arg Cys Lys Pro Val Asn Thr Phe Val His Glu Pro Leu Val
65 70 75 80

Asp Val Gln Asn Val Cys Phe Gln Glu Lys Val Thr Cys Lys Asn Gly
85 90 95

Gln Gly Asn Cys Tyr Lys Ser Asn Ser Ser Met His Ile Thr Asp Cys
100 105 110

Arg Leu Thr Asn Gly Ser Arg Tyr Pro Asn Cys Ala Tyr Arg Thr Ser
115 120 125

Pro Lys Glu Arg His Ile Ile Val Ala Cys Glu Gly Ser Pro Tyr Val
130 135 140

Pro Val His Phe Asp Ala Ser Val Glu Asp Ser Thr
145 150 155

<210> 166
<211> 375
<212> PRT
<213> Human

<400> 166

Met Asp Ala Leu Gln Leu Ala Asn Ser Ala Phe Ala Val Asp Leu Phe
1 5 10 15

Lys Gln Leu Cys Glu Lys Glu Pro Leu Gly Asn Val Leu Phe Ser Pro
20 25 30

Ile Cys Leu Ser Thr Ser Leu Ser Leu Ala Gln Val Gly Ala Lys Gly
35 40 45

Asp Thr Ala Asn Glu Ile Gly Gln Val Leu His Phe Glu Asn Val Lys
50 55 60

Asp Ile Pro Phe Gly Phe Gln Thr Val Thr Ser Asp Val Asn Lys Leu
65 70 75 80

Ser Ser Phe Tyr Ser Leu Lys Leu Ile Lys Arg Leu Tyr Val Asp Lys
85 90 95

Ser Leu Asn Leu Ser Thr Glu Phe Ile Ser Ser Thr Lys Arg Pro Tyr
100 105 110

Ala Lys Glu Leu Glu Thr Val Asp Phe Lys Asp Lys Leu Glu Glu Thr
 115 120 125

Lys Gly Gln Ile Asn Asn Ser Ile Lys Asp Leu Thr Asp Gly His Phe
 130 135 140

Glu Asn Ile Leu Ala Asp Asn Ser Val Asn Asp Gln Thr Lys Ile Leu
 145 150 155 160

Val Val Asn Ala Ala Tyr Phe Val Gly Lys Trp Met Lys Lys Phe Pro
 165 170 175

Glu Ser Glu Thr Lys Glu Cys Pro Phe Arg Leu Asn Lys Thr Asp Thr
 180 185 190

Lys Pro Val Gln Met Met Asn Met Glu Ala Thr Phe Cys Met Gly Asn
 195 200 205

Ile Asp Ser Ile Asn Cys Lys Ile Ile Glu Leu Pro Phe Gln Asn Lys
 210 215 220

His Leu Ser Met Phe Ile Leu Leu Pro Lys Asp Val Glu Asp Glu Ser
 225 230 235 240

Thr Gly Leu Glu Lys Ile Glu Lys Gln Leu Asn Ser Glu Ser Leu Ser
 245 250 255

Gln Trp Thr Asn Pro Ser Thr Met Ala Asn Ala Lys Val Lys Leu Ser
 260 265 270

Ile Pro Lys Phe Lys Val Glu Lys Met Ile Asp Pro Lys Ala Cys Leu
 275 280 285

Glu Asn Leu Gly Leu Lys His Ile Phe Ser Glu Asp Thr Ser Asp Phe
 290 295 300

Ser Gly Met Ser Glu Thr Lys Gly Val Ala Leu Ser Asn Val Ile His
 305 310 315 320

Lys Val Cys Leu Glu Ile Thr Glu Asp Gly Gly Asp Ser Ile Glu Val
 325 330 335

Pro Gly Ala Arg Ile Leu Gln His Lys Asp Glu Leu Asn Ala Asp His
 340 345 350

Pro Phe Ile Tyr Ile Ile Arg His Asn Lys Thr Arg Asn Ile Ile Phe
 355 360 365

Phe Gly Lys Phe Cys Ser Pro
 370 375

<210> 167
 <211> 240
 <212> PRT
 <213> Human

<400> 167

Met Leu Ala Leu Leu Cys Ser Cys Leu Leu Leu Ala Ala Gly Ala Ser
 1 5 10 15

Asp Ala Trp Thr Gly Glu Asp Ser Ala Glu Pro Asn Ser Asp Ser Ala
 20 25 30

Glu Trp Ile Arg Asp Met Tyr Ala Lys Val Thr Glu Ile Trp Gln Glu
 35 40 45

Val Met Gln Arg Arg Asp Asp Asp Gly Thr Leu His Ala Ala Cys Gln
 50 55 60

Val Gln Pro Ser Ala Thr Leu Asp Ala Ala Gln Pro Arg Val Thr Gly
 65 70 75 80

Val Val Leu Phe Arg Gln Leu Ala Pro Arg Ala Lys Leu Asp Ala Phe
 85 90 95

Phe Ala Leu Glu Gly Phe Pro Thr Glu Pro Asn Ser Ser Ser Arg Ala
 100 105 110

Ile His Val His Gln Phe Gly Asp Leu Ser Gln Gly Cys Glu Ser Thr
 115 120 125

Gly Pro His Tyr Asn Pro Leu Ala Val Pro His Pro Gln His Pro Gly
 130 135 140

Asp Phe Gly Asn Phe Ala Val Arg Asp Gly Ser Leu Trp Arg Tyr Arg
 145 150 155 160

Ala Gly Leu Ala Ala Ser Leu Ala Gly Pro His Ser Ile Val Gly Arg
 165 170 175

Ala Val Val Val His Ala Gly Glu Asp Asp Leu Gly Arg Gly Gly Asn
180 185 190

Gln Ala Ser Val Glu Asn Gly Asn Ala Gly Arg Arg Leu Ala Cys Cys
195 200 205

Val Val Gly Val Cys Gly Pro Gly Leu Trp Glu Arg Gln Ala Arg Glu
210 215 220

His Ser Glu Arg Lys Lys Arg Arg Arg Glu Ser Glu Cys Lys Ala Ala
225 230 235 240

<210> 168
<211> 283
<212> PRT
<213> Human

<400> 168

Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
1 5 10 15

Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
20 25 30

Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
35 40 45

Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
50 55 60

Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
65 70 75 80

Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
85 90 95

Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
100 105 110

Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
115 120 125

Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
130 135 140

Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
145 150 155 160

Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
165 170 175

Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala
180 185 190

Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly
195 200 205

Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys
210 215 220

Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser
225 230 235 240

Val Gln Arg Lys Arg Gln Glu Ala Glu Gly Glu Ala Thr Val Ile Glu
245 250 255

Ala Leu Gln Ala Pro Pro Asp Val Thr Thr Val Ala Val Glu Glu Thr
260 265 270

Ile Pro Ser Phe Thr Gly Arg Ser Pro Asn His
275 280

<210> 169
<211> 335
<212> PRT
<213> Human

<400> 169

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
1 5 10 15

Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
20 25 30

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
35 40 45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
50 55 60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65 70 75 80

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
85 90 95

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
100 105 110

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
115 120 125

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
130 135 140

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145 150 155 160

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
165 170 175

Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
180 185 190

Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
195 200 205

Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu
210 215 220

Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met
225 230 235 240

Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu
245 250 255

Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu
260 265 270

Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys
275 280 285

Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys

290

295

300

Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser
 305 310 315 320

Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
 325 330 335

<210> 170
 <211> 207
 <212> PRT
 <213> Human

<400> 170

Met Asn Val Ala Arg Phe Leu Val Glu Lys His Thr Leu His Val Ile
 1 5 10 15

Ile Asp Phe Ile Leu Ser Lys Val Ser Asn Gln Gln Ser Asn Leu Ala
 20 25 30

Gln His Gln Arg Val Tyr Thr Gly Glu Lys Pro Tyr Lys Cys Asn Glu
 35 40 45

Trp Gly Lys Ala Leu Ser Gly Lys Ser Ser Leu Phe Tyr His Gln Ala
 50 55 60

Ile His Gly Val Gly Lys Leu Cys Lys Cys Asn Asp Cys His Lys Val
 65 70 75 80

Phe Ser Asn Ala Thr Thr Ile Ala Asn His Trp Arg Ile His Asn Glu
 85 90 95

Asp Arg Ser Tyr Lys Cys Asn Lys Cys Gly Lys Ile Phe Arg His Arg
 100 105 110

Ser Tyr Leu Ala Val Tyr Gln Arg Thr His Thr Gly Glu Lys Pro Tyr
 115 120 125

Lys Tyr His Asp Cys Gly Lys Val Phe Ser Gln Ala Ser Ser Tyr Ala
 130 135 140

Lys His Arg Arg Ile His Thr Gly Glu Lys Pro His Lys Cys Asp Asp
 145 150 155 160

Cys Gly Lys Val Leu Thr Ser Arg Ser His Leu Ile Arg His Gln Arg

165

170

175

Ile His Thr Gly Gln Lys Ser Tyr Lys Cys Leu Lys Cys Gly Lys Val
 180 185 190

Phe Ser Leu Trp Ala Leu His Ala Glu His Gln Lys Ile His Phe
 195 200 205

<210> 171
 <211> 158
 <212> PRT
 <213> Human

<400> 171

Met Ala Ser Arg Ser Met Arg Leu Leu Leu Leu Leu Ser Cys Leu Ala
 1 5 10 15

Lys Thr Gly Val Leu Gly Asp Ile Ile Met Arg Pro Ser Cys Ala Pro
 20 25 30

Gly Trp Phe Tyr His Lys Ser Asn Cys Tyr Gly Tyr Phe Arg Lys Leu
 35 40 45

Arg Asn Trp Ser Asp Ala Glu Leu Glu Cys Gln Ser Tyr Gly Asn Gly
 50 55 60

Ala His Leu Ala Ser Ile Leu Ser Leu Lys Glu Ala Ser Thr Ile Ala
 65 70 75 80

Glu Tyr Ile Ser Gly Tyr Gln Arg Ser Gln Pro Ile Trp Ile Gly Leu
 85 90 95

His Asp Pro Gln Lys Arg Gln Gln Trp Gln Trp Ile Asp Gly Ala Met
 100 105 110

Tyr Leu Tyr Arg Ser Trp Ser Gly Lys Ser Met Gly Gly Asn Lys His
 115 120 125

Cys Ala Glu Met Ser Ser Asn Asn Asn Phe Leu Thr Trp Ser Ser Asn
 130 135 140

Glu Cys Asn Lys Arg Gln His Phe Leu Cys Lys Tyr Arg Pro
 145 150 155

<210> 172

<211> 432
 <212> PRT
 <213> Human

<400> 172

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Met Gly Pro Ala Gly Ser Leu Leu Gly Ser Gly Gln Met Gln Ile Thr
1          5          10          15

Leu Trp Gly Ser Leu Ala Ala Val Ala Ile Phe Phe Val Ile Thr Phe
          20          25          30

Leu Ile Phe Pro Cys Ser Ser Cys Asp Arg Glu Lys Lys Pro Arg Gln
          35          40          45

His Ser Gly Asp His Glu Asn Leu Met Asn Val Pro Ser Asp Lys Glu
          50          55          60

Met Phe Ser Arg Ser Val Thr Ser Leu Ala Thr Asp Ala Pro Ala Ser
65          70          75          80

Ser Glu Gln Asn Gly Ala Leu Thr Asn Gly Asp Ile Leu Ser Glu Asp
          85          90          95

Ser Thr Leu Thr Cys Met Gln His Tyr Glu Glu Val Gln Thr Ser Ala
          100          105          110

Ser Asp Leu Leu Asp Ser Gln Asp Ser Thr Gly Lys Pro Lys Cys His
          115          120          125

Gln Ser Arg Glu Leu Pro Arg Ile Pro Pro Glu Ser Ala Val Asp Thr
          130          135          140

Met Leu Thr Ala Arg Ser Val Asp Gly Asp Gln Gly Leu Gly Met Glu
145          150          155          160

Gly Pro Tyr Glu Val Leu Lys Asp Ser Ser Ser Gln Glu Asn Met Val
          165          170          175

Glu Asp Cys Leu Tyr Glu Thr Val Lys Glu Ile Lys Glu Val Ala Ala
          180          185          190

Ala Ala His Leu Glu Lys Gly His Ser Gly Lys Ala Lys Ser Thr Ser
          195          200          205

Ala Ser Lys Glu Leu Pro Gly Pro Gln Thr Glu Gly Lys Ala Glu Phe

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210 215 220
 Ala Glu Tyr Ala Ser Val Asp Arg Asn Lys Lys Cys Arg Gln Ser Val
 225 230 235 240
 Asn Val Glu Ser Ile Leu Gly Asn Ser Cys Asp Pro Glu Glu Glu Ala
 245 250 255
 Pro Pro Pro Val Pro Val Lys Leu Leu Asp Glu Asn Glu Asn Leu Gln
 260 265 270
 Glu Lys Glu Gly Gly Glu Ala Glu Glu Ser Ala Thr Asp Thr Thr Ser
 275 280 285
 Glu Thr Asn Lys Arg Phe Ser Ser Leu Ser Tyr Lys Ser Arg Glu Glu
 290 295 300
 Asp Pro Thr Leu Thr Glu Glu Glu Ile Ser Ala Met Tyr Ser Ser Val
 305 310 315 320
 Asn Lys Pro Gly Gln Leu Val Asn Lys Ser Gly Gln Ser Leu Thr Val
 325 330 335
 Pro Glu Ser Thr Tyr Thr Ser Ile Gln Gly Asp Pro Gln Arg Ser Pro
 340 345 350
 Ser Ser Cys Asn Asp Leu Tyr Ala Thr Val Lys Asp Phe Glu Lys Thr
 355 360 365
 Pro Asn Ser Thr Leu Pro Pro Ala Gly Arg Pro Ser Glu Glu Pro Glu
 370 375 380
 Pro Asp Tyr Glu Ala Ile Gln Thr Leu Asn Arg Glu Glu Glu Lys Ala
 385 390 395 400
 Thr Leu Gly Thr Asn Gly His His Gly Leu Val Pro Lys Glu Asn Asp
 405 410 415
 Tyr Glu Ser Ile Ser Asp Leu Gln Gln Gly Arg Asp Ile Thr Arg Leu
 420 425 430

<210> 173
 <211> 174
 <212> PRT
 <213> Human

<400> 173

Lys Pro Phe Arg Cys Glu Asn Cys Asn Glu Arg Phe Gln Tyr Lys Tyr
 1 5 10 15

Gln Leu Arg Ser His Met Ser Ile His Ile Gly His Lys Gln Phe Met
 20 25 30

Cys Gln Trp Cys Gly Lys Asp Phe Asn Met Lys Gln Tyr Phe Asp Glu
 35 40 45

His Met Lys Thr His Thr Gly Glu Lys Pro Tyr Ile Cys Glu Ile Cys
 50 55 60

Gly Lys Ser Phe Thr Ser Arg Pro Asn Met Lys Arg His Arg Arg Thr
 65 70 75 80

His Thr Gly Glu Lys Pro Tyr Pro Cys Asp Val Cys Gly Gln Arg Phe
 85 90 95

Arg Phe Ser Asn Met Leu Lys Ala His Lys Glu Lys Cys Phe Arg Val
 100 105 110

Ser His Thr Leu Ala Gly Asp Gly Val Pro Ala Ala Pro Gly Leu Pro
 115 120 125

Pro Thr Gln Pro Gln Ala His Ala Leu Pro Leu Leu Pro Gly Leu Pro
 130 135 140

Gln Thr Leu Pro Pro Pro Pro His Leu Pro Pro Pro Pro Pro Leu Phe
 145 150 155 160

Pro Thr Thr Ala Ser Pro Gly Gly Arg Met Asn Ala Asn Asn
 165 170

<210> 174

<211> 917

<212> PRT

<213> Human

<400> 174

Ala Ser Pro Arg Gly Thr Glu Ala Ser Pro Pro Gln Asn Asn Ser Gly
 1 5 10 15

Ser Ser Ser Pro Val Phe Thr Phe Arg His Pro Leu Leu Ser Ser Gly

20						25						30					
Gly	Pro	Gln	Ser	Pro	Leu	Arg	Gly	Ser	Thr	Gly	Ser	Leu	Lys	Ser	Ser		
		35					40					45					
Pro	Ser	Met	Ser	His	Met	Glu	Ala	Leu	Gly	Lys	Ala	Trp	Asn	Arg	Gln		
	50					55					60						
Leu	Ser	Arg	Pro	Leu	Ser	Gln	Ala	Val	Ser	Phe	Ser	Thr	Pro	Phe	Gly		
65					70					75					80		
Leu	Asp	Ser	Asp	Val	Asp	Val	Val	Met	Gly	Asp	Pro	Val	Leu	Leu	Arg		
				85					90					95			
Ser	Val	Ser	Ser	Asp	Ser	Leu	Gly	Pro	Pro	Arg	Pro	Ala	Pro	Ala	Arg		
			100					105					110				
Thr	Pro	Thr	Gln	Pro	Pro	Pro	Glu	Pro	Gly	Asp	Leu	Pro	Thr	Ile	Glu		
		115					120					125					
Glu	Ala	Leu	Gln	Ile	Ile	His	Ser	Ala	Glu	Pro	Arg	Leu	Leu	Pro	Asp		
	130					135					140						
Gly	Ala	Ala	Asp	Gly	Ser	Phe	Tyr	Leu	His	Ser	Pro	Glu	Gly	Pro	Ser		
145					150					155					160		
Lys	Pro	Ser	Leu	Ala	Ser	Pro	Tyr	Leu	Pro	Glu	Gly	Thr	Ser	Lys	Pro		
			165						170					175			
Leu	Ser	Asp	Arg	Pro	Thr	Lys	Ala	Pro	Val	Tyr	Met	Pro	His	Pro	Glu		
			180					185					190				
Thr	Pro	Ser	Lys	Pro	Ser	Pro	Cys	Leu	Val	Gly	Glu	Ala	Ser	Lys	Pro		
		195					200					205					
Pro	Ala	Pro	Ser	Glu	Gly	Ser	Pro	Lys	Ala	Val	Ala	Ser	Ser	Pro	Ala		
	210					215					220						
Ala	Thr	Asn	Ser	Glu	Val	Lys	Met	Thr	Ser	Phe	Ala	Glu	Arg	Lys	Lys		
225					230					235					240		
Gln	Leu	Val	Lys	Ala	Glu	Ala	Glu	Ala	Gly	Ala	Gly	Ser	Pro	Thr	Ser		
				245					250					255			

Thr Pro Ala Pro Pro Glu Ala Leu Ser Ser Glu Met Ser Glu Leu Ser
 260 265 270

Ala Arg Leu Glu Glu Lys Arg Arg Ala Ile Glu Ala Gln Lys Arg Arg
 275 280 285

Ile Glu Ala Ile Phe Ala Lys His Arg Gln Arg Leu Gly Lys Ser Ala
 290 295 300

Phe Leu Gln Val Gln Pro Arg Glu Ala Ser Gly Glu Ala Glu Ala Glu
 305 310 315 320

Ala Glu Glu Ala Asp Ser Gly Pro Val Pro Gly Gly Glu Arg Pro Ala
 325 330 335

Gly Glu Gly Gln Gly Glu Pro Thr Ser Arg Pro Lys Ala Val Thr Phe
 340 345 350

Ser Pro Asp Leu Gly Pro Val Pro His Glu Gly Leu Gly Glu Tyr Asn
 355 360 365

Arg Ala Val Ser Lys Leu Ser Ala Ala Leu Ser Ser Leu Gln Arg Asp
 370 375 380

Met Gln Arg Leu Thr Asp Gln Gln Gln Arg Leu Leu Ala Pro Pro Glu
 385 390 395 400

Ala Pro Gly Ser Ala Pro Pro Pro Ala Ala Trp Val Ile Pro Gly Pro
 405 410 415

Thr Thr Gly Pro Lys Ala Ala Ser Pro Ser Pro Ala Arg Arg Val Pro
 420 425 430

Ala Thr Arg Arg Ser Pro Gly Pro Gly Pro Ser Gln Ser Pro Arg Ser
 435 440 445

Pro Lys His Thr Arg Pro Ala Glu Leu Arg Leu Ala Pro Leu Thr Arg
 450 455 460

Val Leu Thr Pro Pro His Asp Val Asp Ser Leu Pro His Leu Arg Lys
 465 470 475 480

Phe Ser Pro Ser Gln Val Pro Val Gln Thr Arg Ser Ser Ile Leu Leu
 485 490 495

Ala Glu Glu Thr Pro Pro Glu Glu Pro Ala Ala Arg Pro Gly Leu Ile
 500 505 510

Glu Ile Pro Leu Gly Ser Leu Ala Asp Pro Ala Ala Glu Asp Glu Gly
 515 520 525

Asp Gly Ser Pro Ala Gly Ala Glu Asp Ser Leu Glu Glu Glu Ala Ser
 530 535 540

Ser Glu Gly Glu Pro Arg Val Gly Leu Gly Phe Phe Tyr Lys Asp Glu
 545 550 555 560

Asp Lys Pro Glu Asp Glu Met Ala Gln Lys Arg Ala Ser Leu Leu Glu
 565 570 575

Arg Gln Gln Arg Arg Ala Glu Glu Ala Arg Arg Arg Lys Gln Trp Gln
 580 585 590

Glu Val Glu Lys Glu Gln Arg Arg Glu Glu Ala Ala Arg Leu Ala Gln
 595 600 605

Glu Glu Ala Pro Gly Pro Ala Pro Leu Val Ser Ala Val Pro Met Ala
 610 615 620

Thr Pro Ala Pro Ala Ala Arg Ala Pro Ala Glu Glu Glu Val Gly Pro
 625 630 635 640

Arg Lys Gly Asp Phe Thr Arg Gln Glu Tyr Glu Arg Arg Ala Gln Leu
 645 650 655

Lys Leu Met Asp Asp Leu Asp Lys Val Leu Arg Pro Arg Ala Ala Gly
 660 665 670

Ser Gly Gly Pro Gly Arg Gly Gly Arg Arg Ala Thr Arg Pro Arg Ser
 675 680 685

Gly Cys Cys Asp Asp Ser Ala Leu Ala Arg Ser Pro Ala Arg Gly Leu
 690 695 700

Leu Gly Ser Arg Leu Ser Lys Ile Tyr Ser Gln Ser Thr Leu Ser Leu
 705 710 715 720

Ser Thr Val Ala Asn Glu Ala His Asn Asn Leu Gly Val Lys Arg Pro
 725 730 735

Thr Ser Arg Ala Pro Ser Pro Ser Gly Leu Met Ser Pro Ser Arg Leu
 740 745 750

Pro Gly Ser Arg Glu Arg Asp Trp Glu Asn Gly Ser Asn Ala Ser Ser
 755 760 765

Pro Ala Ser Val Pro Glu Tyr Thr Gly Pro Arg Leu Tyr Lys Glu Pro
 770 775 780

Ser Ala Lys Ser Asn Lys Phe Ile Ile His Asn Ala Leu Ser His Cys
 785 790 795 800

Cys Leu Ala Gly Lys Val Asn Glu Pro Gln Lys Asn Arg Ile Leu Glu
 805 810 815

Glu Ile Glu Lys Ser Lys Ala Asn His Phe Leu Ile Leu Phe Arg Asp
 820 825 830

Ser Ser Cys Gln Phe Arg Ala Leu Tyr Thr Leu Ser Gly Glu Thr Glu
 835 840 845

Glu Leu Ser Arg Leu Ala Gly Tyr Gly Pro Arg Thr Val Thr Pro Ala
 850 855 860

Met Val Glu Gly Ile Tyr Lys Tyr Asn Ser Asp Arg Lys Arg Phe Thr
 865 870 875 880

Gln Ile Pro Ala Lys Thr Met Ser Met Ser Val Asp Ala Phe Thr Ile
 885 890 895

Gln Gly His Leu Trp Gln Gly Lys Lys Pro Thr Thr Pro Lys Lys Gly
 900 905 910

Gly Gly Thr Pro Lys
 915

<210> 175
 <211> 600
 <212> PRT
 <213> Human

<400> 175

Met Arg Ser Cys Leu Trp Arg Cys Arg His Leu Ser Gln Gly Val Gln
 1 5 10 15

Trp Ser Leu Leu Leu Ala Val Leu Val Phe Phe Leu Phe Ala Leu Pro
 20 25 30

Ser Phe Ile Lys Glu Pro Gln Thr Lys Pro Ser Arg His Gln Arg Thr
 35 40 45

Glu Asn Ile Lys Glu Arg Ser Leu Gln Ser Leu Ala Lys Pro Lys Ser
 50 55 60

Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile Tyr Ala Glu Pro Val
 65 70 75 80

Pro Glu Asn Asn Ala Leu Asn Thr Gln Thr Gln Pro Lys Ala His Thr
 85 90 95

Thr Gly Asp Arg Gly Lys Glu Ala Asn Gln Ala Pro Pro Glu Glu Gln
 100 105 110

Asp Lys Val Pro His Thr Ala Gln Arg Ala Ala Trp Lys Ser Pro Glu
 115 120 125

Lys Glu Lys Thr Met Val Asn Thr Leu Ser Pro Arg Gly Gln Asp Ala
 130 135 140

Gly Met Ala Ser Gly Arg Thr Glu Ala Gln Ser Trp Lys Ser Gln Asp
 145 150 155 160

Thr Lys Thr Thr Gln Gly Asn Gly Gly Gln Thr Arg Lys Leu Thr Ala
 165 170 175

Ser Arg Thr Val Ser Glu Lys His Gln Gly Lys Ala Ala Thr Thr Ala
 180 185 190

Lys Thr Leu Ile Pro Lys Ser Gln His Arg Met Leu Ala Pro Thr Gly
 195 200 205

Ala Val Ser Thr Arg Thr Arg Gln Lys Gly Val Thr Thr Ala Val Ile
 210 215 220

Pro Pro Lys Glu Lys Lys Pro Gln Ala Thr Pro Pro Pro Ala Pro Phe
 225 230 235 240

Gln Ser Pro Thr Thr Gln Arg Asn Gln Arg Leu Lys Ala Ala Asn Phe

					245						250						255
Lys	Ser	Glu	Pro	Arg	Trp	Asp	Phe	Glu	Glu	Lys	Tyr	Ser	Phe	Glu	Ile		
			260					265					270				
Gly	Gly	Leu	Gln	Thr	Thr	Cys	Pro	Asp	Ser	Val	Lys	Ile	Lys	Ala	Ser		
		275					280					285					
Lys	Ser	Leu	Trp	Leu	Gln	Lys	Leu	Phe	Leu	Pro	Asn	Leu	Thr	Leu	Phe		
	290					295					300						
Leu	Asp	Ser	Arg	His	Phe	Asn	Gln	Ser	Glu	Trp	Asp	Arg	Leu	Glu	His		
305					310					315					320		
Phe	Ala	Pro	Pro	Phe	Gly	Phe	Met	Glu	Leu	Asn	Tyr	Ser	Leu	Val	Gln		
				325					330					335			
Lys	Val	Val	Thr	Arg	Phe	Pro	Pro	Val	Pro	Gln	Gln	Gln	Leu	Leu	Leu		
			340					345					350				
Ala	Ser	Leu	Pro	Ala	Gly	Ser	Leu	Arg	Cys	Ile	Thr	Cys	Ala	Val	Val		
		355					360					365					
Gly	Asn	Gly	Gly	Ile	Leu	Asn	Asn	Ser	His	Met	Gly	Gln	Glu	Ile	Asp		
	370					375					380						
Ser	His	Asp	Tyr	Val	Phe	Arg	Leu	Ser	Gly	Ala	Leu	Ile	Lys	Gly	Tyr		
385					390					395					400		
Glu	Gln	Asp	Val	Gly	Thr	Arg	Thr	Ser	Phe	Tyr	Gly	Phe	Thr	Ala	Phe		
				405					410					415			
Ser	Leu	Thr	Gln	Ser	Leu	Leu	Ile	Leu	Gly	Asn	Arg	Gly	Phe	Lys	Asn		
			420					425					430				
Val	Pro	Leu	Gly	Lys	Asp	Val	Arg	Tyr	Leu	His	Phe	Leu	Glu	Gly	Thr		
		435					440					445					
Arg	Asp	Tyr	Glu	Trp	Leu	Glu	Ala	Leu	Leu	Met	Asn	Gln	Thr	Val	Met		
	450					455					460						
Ser	Lys	Asn	Leu	Phe	Trp	Phe	Arg	His	Arg	Pro	Gln	Glu	Ala	Phe	Arg		
465					470					475					480		

Glu Ala Leu His Met Asp Arg Tyr Leu Leu Leu His Pro Asp Phe Leu
 485 490 495

Arg Tyr Met Lys Asn Arg Phe Leu Arg Ser Lys Thr Leu Asp Gly Ala
 500 505 510

His Trp Arg Ile Tyr Arg Pro Thr Thr Gly Ala Leu Leu Leu Leu Thr
 515 520 525

Ala Leu Gln Leu Cys Asp Gln Val Ser Ala Tyr Gly Phe Ile Thr Glu
 530 535 540

Gly His Glu Arg Phe Ser Asp His Tyr Tyr Asp Thr Ser Trp Lys Arg
 545 550 555 560

Leu Ile Phe Tyr Ile Asn His Asp Phe Lys Leu Glu Arg Glu Val Trp
 565 570 575

Lys Arg Leu His Asp Glu Gly Ile Ile Arg Leu Tyr Gln Arg Pro Gly
 580 585 590

Pro Gly Thr Ala Lys Ala Lys Asn
 595 600

<210> 176
 <211> 312
 <212> PRT
 <213> Human

<400> 176

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1 5 10 15

Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser
 20 25 30

Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
 35 40 45

Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60

Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
 65 70 75 80

Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
85 90 95

Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
100 105 110

Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Leu Cys Lys
115 120 125

Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
130 135 140

Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
145 150 155 160

Ala Phe Leu Val Asn Leu Ala Phe Cys Gly Pro Asn Val Leu Asp Ser
165 170 175

Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg Leu Ala Cys Thr Asp Thr
180 185 190

Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
195 200 205

Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Val Phe Ile Leu Phe Thr
210 215 220

Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
225 230 235 240

Ser Ala His Ser Thr Val Val Leu Leu Phe Phe Gly Pro Pro Met Phe
245 250 255

Val Tyr Thr Arg Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
260 265 270

Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
275 280 285

Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
290 295 300

Leu Val Ile Tyr Lys Arg Ile Ser
305 310

<210> 177
 <211> 114
 <212> PRT
 <213> Human

<400> 177

Met Ala Leu Glu His Leu Val Val Trp His Val His Ser Glu Asp Gln
 1 5 10 15

Ser Phe Val Val Leu Lys Thr Asp Leu Gly Arg Arg Gly Cys Arg Pro
 20 25 30

Leu Arg Lys Thr Ala Pro Lys Ala Lys Glu Ala Pro Ala Pro Pro Lys
 35 40 45

Ala Glu Ala Lys Val Lys Ala Leu Lys Ala Lys Lys Ala Val Leu Lys
 50 55 60

Gly Val Arg Ser His Thr Gln Lys Arg Arg Ser Ala Cys His Ser Pro
 65 70 75 80

Ser Gly Gly Pro Arg His Cys Asp Ser Gly Gly Ser Pro Asp Ile Leu
 85 90 95

Gly Arg Ala Pro Pro Gly Glu Thr Ser Leu Ala Thr Met Leu Ser Ser
 100 105 110

Phe Arg

<210> 178
 <211> 430
 <212> PRT
 <213> Human

<400> 178

Asp Ser Met Thr Phe Glu Asp Ile Ile Val Asp Phe Thr Gln Glu Glu
 1 5 10 15

Trp Ala Leu Leu Asp Thr Ser Gln Arg Lys Leu Phe Gln Asp Val Met
 20 25 30

Leu Glu Asn Ile Ser His Leu Val Ser Ile Gly Glu Asp Phe Thr Gln
 35 40 45

His Ile Ala Leu Thr Gln Asn Val Ile Thr Tyr Met Arg Thr Lys His
50 55 60

Phe Val Ser Lys Lys Phe Gly Lys Ile Phe Ser Asp Trp Leu Ser Phe
65 70 75 80

Asn Gln His Lys Glu Ile His Thr Lys Cys Lys Ser Tyr Gly Ser His
85 90 95

Leu Phe Asp Tyr Ala Phe Ile Gln Asn Ser Ala Leu Arg Pro His Ser
100 105 110

Val Thr His Thr Arg Glu Ile Thr Leu Glu Cys Arg Val Cys Gly Lys
115 120 125

Thr Phe Ser Lys Asn Ser Asn Leu Arg Arg His Glu Met Ile His Thr
130 135 140

Gly Glu Lys Pro His Gly Cys His Leu Cys Gly Lys Ala Phe Thr His
145 150 155 160

Cys Ser Asp Leu Arg Lys His Glu Arg Thr His Thr Gly Glu Lys Pro
165 170 175

Tyr Gly Cys His Leu Cys Gly Lys Ala Phe Ser Lys Ser Ser Asn Leu
180 185 190

Arg Arg His Glu Met Ile His Thr Arg Glu Lys Ala Gln Ile Cys His
195 200 205

Leu Cys Gly Lys Ala Phe Thr His Cys Ser Asp Leu Arg Lys His Glu
210 215 220

Arg Thr His Leu Gly Asp Lys Pro Tyr Gly Cys Leu Leu Cys Gly Lys
225 230 235 240

Ala Phe Ser Lys Cys Ser Tyr Leu Arg Gln His Glu Arg Thr His Asn
245 250 255

Gly Glu Lys Pro Tyr Glu Cys His Leu Cys Gly Lys Ala Phe Ser His
260 265 270

Cys Ser His Leu Arg Gln His Glu Arg Ser His Asn Gly Glu Lys Pro
275 280 285

His Gly Cys His Leu Cys Gly Lys Ala Phe Thr Glu Ser Ser Val Leu
 290 295 300

Lys Arg His Glu Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys His
 305 310 315 320

Val Cys Gly Lys Ala Phe Thr Glu Ser Ser Asp Leu Arg Arg His Glu
 325 330 335

Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys His Leu Cys Gly Lys
 340 345 350

Ala Phe Asn His Ser Ser Val Leu Arg Arg His Glu Arg Thr His Thr
 355 360 365

Gly Glu Lys Pro Tyr Glu Cys Asn Ile Cys Gly Lys Ala Phe Asn Arg
 370 375 380

Ser Tyr Asn Phe Arg Leu His Arg Arg Val His Thr Gly Glu Lys Pro
 385 390 395 400

Tyr Val Cys Pro Leu Cys Gly Lys Ala Phe Ser Lys Phe Phe Asn Leu
 405 410 415

Arg Gln His Glu Arg Thr His Thr Lys Lys Ala Met Asn Met
 420 425 430

<210> 179
 <211> 15
 <212> DNA
 <213> Murine

<400> 179
 aactatggtg tacac

15

<210> 180
 <211> 5
 <212> PRT
 <213> Murine

<400> 180

Asn Tyr Gly Val His
 1 5

<210> 181
 <211> 48

<212> DNA
<213> Murine

<400> 181
gtgatatgga gtggtggaaa cacagactat aatacacctt tcacatcc 48

<210> 182
<211> 16
<212> PRT
<213> Murine

<400> 182
Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser
1 5 10 15

<210> 183
<211> 33
<212> DNA
<213> Murine

<400> 183
gccctcacct actatgatta cgagtttgct tac 33

<210> 184
<211> 11
<212> PRT
<213> Murine

<400> 184
Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr
1 5 10

<210> 185
<211> 33
<212> DNA
<213> Murine

<400> 185
agggccagtc agagtattgg cacaaacata cac 33

<210> 186
<211> 11
<212> PRT
<213> Murine

<400> 186
Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His
1 5 10

<210> 187

<211> 18
<212> DNA
<213> Murine

<400> 187
gcttctgagt ctatctct

18

<210> 188
<211> 6
<212> PRT
<213> Murine

<400> 188

Ala Ser Glu Ser Ile Ser
1 5

<210> 189
<211> 27
<212> DNA
<213> Murine

<400> 189
caacaaaata ataactggcc aaccacg

27

<210> 190
<211> 9
<212> PRT
<213> Murine

<400> 190

Gln Gln Asn Asn Asn Trp Pro Thr Thr
1 5

<210> 191
<211> 17
<212> DNA
<213> Artificial

<220>
<223> GAPDH oligonucleotide

<400> 191
agccgagcca catcgct

17

<210> 192
<211> 19
<212> DNA
<213> Artificial

<220>
<223> GAPDH oligonucleotide

<400> 192
gtgaccaggc gcccaatac 19

<210> 193
<211> 19
<212> DNA
<213> Artificial

<220>
<223> EGFR oligonucleotide

<400> 193
gcgtctcttg ccggaatgt 19

<210> 194
<211> 21
<212> DNA
<213> Artificial

<220>
<223> EGFR oligonucleotide

<400> 194
agccgaggca gggaatgcgt g 21